#007 /C:/7:60 6T שבי סכר

18-10-658-989a-7.rad

rage

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model Run on:

; Search time 97.3985 Seconds (without alignments) 2272.479 Million cell updates/sec October 18, 2004, 13:22:25

US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGG.....GEQGVPGDLGAPGPSGPAGG

Title: Perfect score: Sequence:

Scoring table:

617

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*
1. geneseqp1980s:\*
2. geneseqp1990s:\*
3. geneseqp2001s:\*
5. geneseqp2001s:\*
6. geneseqp2003s:\*
7. geneseqp2003bs:\*
8. geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|               |        | de     |          |    |          |                    |
|---------------|--------|--------|----------|----|----------|--------------------|
| Result<br>No. | Score  |        | Length   | ОВ |          | Description        |
| 1             | 3488   | 00.    | 617      | ao | ADM48391 | Adm48391 Human rec |
| N             |        | 100.0  | 617      | ω  |          | 9                  |
| m             | 48     | φ.     | 821      | യ  | σ        | 92 Human           |
| 4             | 237.   | 4.     | 1057     | ო  | AAY84544 | ര                  |
| Ŋ             | 237.   | 4.     | О        | m  | AAY84403 | 403 Amino ac       |
| 9             | ٠      | 4.     | 1107     | m  | AAY84540 | 10                 |
| 7             | 237.   | 4,     | $\vdash$ | ო  | AAY84538 | 538 A chimer       |
| œ             | 237.   | 4.     | 4        | ~1 | AAW68485 | Aaw68485 Human rec |
| σ             | 237.   | 4.     | 4        | 7  | ADD45059 | Add45059 Human Pro |
| 10            | 237.   | 4.     | 1464     | 7  | ADD45055 | Add45055 Human Pro |
| 11            | 237.   | 4.     | 1464     | ۲  | 50       | Add45051 Human Pro |
| 12            | 23     | 4.     | 1449     | 4  | AAE02535 | Aae02535 Porcine a |
| 13            | 233.   | 4.     | 9        | 7  | 05       | )50 Human          |
| 14            | 2233.5 | 4.     | 1461     | Ŋ  | ABG93947 | Abg93947 Human pol |
| 15            | 233.   | 4.     | 46       | 4  | m        | .36 Human          |
| 16            | 233.   | 4.     | 53       | 7  | ADE87051 | 151 Human pa:      |
| 17            | 231.   | 4.     | 05       | ო  | 4        | 541 Amino          |
| 18            | 229.   | ო      | 38       | m  | AAY84539 | 339                |
| 19            | 228.   | m      | 34       | C) | AAR71701 | 701                |
| 20            | 228.   | ش      | 4        | ო  | 512      | Aay96122 Collagen  |
| 21            | 228.   | ო      | 1341     | 'n | AAE16475 | 5475               |
| 22            | 228.   | e.     | 4        | w  | ABB80733 | Abb80733 Collagen  |
| 23            | 228.   | m<br>m | 4        | Ŋ  | 2        | 625 Amino          |
| 24            | 228.   |        | 1341     | 7  | F1307    | ~                  |
| 25            | 227.   | ë.     | 9        | 41 | AAB82454 | Aab82454 Human pro |

| Human Tum | Human pan | Human tum | Breast ca | Human cer | Human src | Human alp | Human sof | Bovine al | Human pan | Collagen/ | Collagen/ | Amino aci | Collagen/ | Collagen/  | Human pan | Human pan | Human pre | Rat Prote | Rat Prote |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|
| Abb90764  | Abp68610  | Abu54471  | Abr47417  |           | Add14142  | Adp65246  | Adq19470  |           | Ade87048  | Aar89472  | Aar89469  | Aay84537  | Aar89470  | - Aar89471 | Ade87057  | Ade87062  | Aay56800  | Add45053  | Add45057  |
| 9076      | ABP68610  | ABU54471  | ABR47417  | ABR92064  | 1414      | ADP65246  | 947       | S         | 3704      | 947       | AAR89469  | AAY84537  | AAR89470  | AAR89471   | ADE87057  | ADE87062  | AAY56800  | ADD45053  | ADD45057  |
| 'n        | ហ         | 9         | w         | w         | ۲-        | 1         | ω         | 4         | 1         | N         | N         | m         | N         | N          | 1         | 7         | m         | 7         | <b>!~</b> |
| 9         | 1464      | 9         | 1464      | 1464      | 1464      | 1464      | 1464      | 1463      | 1464      | 1107      | 1169      | 1169      | 1171      | 1388       | 1211      | 1226      | 1411      | 1453      | 1453      |
| 63.9      | 63.8      | 3         | m         | 63.8      | S)        | m         | 63.8      | 3         | 3         | S         | m         | 63.7      | 63.7      | m          | m         | 63.7      | 3         | 63.5      | 63.5      |
| 22        | 2227.5    | 2         | 22        | 2227.5    | 2227.5    | 2227.5    | 2227.5    | 'n        | 2224.5    | 222.      | 22        | 2222.5    | 22        |            | 22        |           | 22        | 2215.5    | S         |
|           | 27        |           |           |           | 31        | 32        | 33        | 34        |           | 36        | 37        | 38        | 39        |            | 41        | 42        | 43        | 44        | 45        |

## ALIGNMENTS

substitute; Gelatin-like protein; plasma expander; human. Human recombinant gelatin-like polypeptide Hu-3. ADM48391 standard; protein; 617 AA. (first entry) Homo sapiens, EP1398324-A1 03-JUN-2004 ADM48391; Plasma RESULT 1 ADM48391 

17-MAR-2004.

11-SEP-2002; 2002EP-00078745. 11-SEP-2002; 2002EP-00078745

Β.

(FUJF ) FUJI PHOTO FILM

Toda Y; WPI; 2004-229415/22. Bouwstra JB,

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.

Example 1; SEQ ID NO 2; 31pp; English.

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a trimer of human recombinant gelatin-like protein Hu-1 hDM48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kDa and at most 50 kDa and an isoelectric point of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate protein, is useful as a plasma expander that has a lower clearance rate clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-like proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically

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GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 120
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 WO2004056976-A2
                            08-JUL-2004
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active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstituin. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as hormones.
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Gaps

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Length 617; Indels

100.0%; Score 3488; DB 8; 100.0%; Pred. No. 1.7e-207; ive 0; Mismatches 0;

120

9

240

180

300

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Like polypeptide Hu-3, which has a molecular weight of approximately 54 kba and which contains multiple Gly Xaa-Yaa triplets. In an example from the invention, recombinant Hu-3 was immobilised on polystynene beads using a heterobifunctional crosslinking agent, and used in a spinner flask cell culture. A claimed process for the preparation of a cell culture support comprises the step of coating a microcarrier bead with gelatine or gelatine-like protein having a molecular weight of about 40-200 kba, and optionally further comprising the step of immobilising the gelatine or gelatine-like protein on the microcarrier. In this process, of the gelatine or gelatine-like protein has the same molecular weight. The gelatine or gelatine-like protein is recombinantly produced to obtain a material of uniform molecular weight and to reduce the risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing cell culture support useful for culturing anchorage dependent cells, involves coating microcarrier bead with gelatine or gelatine-like protein having specific molecular weight.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is the protein sequence of human recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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                                                                                                                                                                                                     Toda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 1; 19pp;
                                                                      23-DEC-2002; 2002EP-00080539
2003WO-NL000922
                                                                                                                                                                                                     Es AJJ,
                                                                                                                                     PHOTO FILM
                                                                                                                                                                                                                                                                        WPI; 2004-507711/48.
                                                                                                                                  (FUJF ) FUJI
   23-DEC-2003;
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gelatin

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-1 Any48390. A claimed composition suitable as a substitute for protein Hu-1 Any48390. A claimed composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid composition. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 kPa and at most 50 kDa and an cost 50 kDa and an coupled and compounds. The protein, or a dimer, trimer or compounds. The proteins can be covalently attached to continue the coupled antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the circulating a more constant plasma level of the medicament. Suitable 420 480 480 540 540 900 saline GSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGAGAGWMGFPGPKGAAGEPGKAGERGVP GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQ GPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGSPGGLPGPPGBAGPPGEAGKPGEQ *GPAGERGEQGPAGSPGFQGLPGPAGPPGEAGXPGEQGVPGDLGAPGPSGPAGEPGPTGLP* GPAGERGEOGPAGSPGFOGLPGPPGBAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLP GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP GPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLT Composition useful as substitute for plasma, comprises solution of st and recombinant gelatin-like protein having colloid osmotic function. Plasma substitute; Gelatin-like protein; plasma expander; human. Human recombinant gelatin-like polypeptide Hu-4. Example 1; SEQ ID NO 3; 31pp; English. Ā ADM48392 standard; protein; 821 GVPGDLGAPGPSGPAGG 617 11-SEP-2002; 2002EP-00078745 11-SEP-2002; 2002EP-00078745 GVPGDLGAPGPSGPAGG (FUJF ) FUJI PHOTO FILM χ, WPI; 2004-229415/22. Toda EP1398324-A1. Bouwstra JB, 17-MAR-2004 03-JUN-2004 421 ( 361 541 ADM48392 361 421 481 481 541 601 601 Homo RESULT 3 ADM48392 g 엄 ò 엄 8 엄 ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.
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                                                                                                                                                                                                                      121 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                                                                                                                                                                                                                                                      241 GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGSPGKTGPPGPAGDGRP
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                                                                                             GPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
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                                                                     GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
                                                                                                                                                                                          GEPGKAGERGVPGPPGAVGPACKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
                                         Gaps
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                                         0; Indels
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           Score 3482; DB 8; L
Pred. No. 4.9e-207;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84544 standard; protein; 1057 AA
99.8%; Scc.
100.0%; Pre
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Best Local Similarity
Matches 616; Conserv
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medicaments include those involved in intervening blood clotting, vasodilation, function of erythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as

Sequence 821 AA;

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957 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1016
                                                                                                                                                                                                                                                                        GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPPF 510
                                                                                                                                                                                                                                                                                                          GPAGKSGDRGETGPAGPAGPAGARGPAGPRGPRGDKGETGEQGDRGIKGHRGFSGLQ 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
557 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human type 1 (alpha1) collagen protein. epptides derived from the protien were used to demonstrate incorporation of 3,4-dehydro-L-prolline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting at least one 3,4-dehydroprolle residue in the polypeptide with an epoxidation reagent from a polypeptide containing at least one 3,4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incorporating non-natural amino acid into polypeptide, useful e.g. for production of bloadhesives, by epoxidation or substitution of dehydroproline residues.
                                                                                                          717 GAAGRVGPPGPSGNAGPPGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                             Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bioadhesive.
                                                      ----VGPAGKDGEAGAQGPPGPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                              394 GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                                  GARGOAGVMGFPGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of human type 1 (alphal) collagen polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY84403 standard; protein; 1058 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buechter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US020462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLGAPGPSGPAG
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BUECHTER D D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-271051/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a method for producing an extracellular matrix procein or its fragment. The extracellular matrix procein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibringen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The presents requence represents human collagen is alphatoal region, which may be accenting the presents of proceins and function of presents enemethod is also useful in studying the structure and function of presents enemethod is also useful in studying the structure and function of presents enemethod is also useful in studying the structure and function of presents enemethod is also useful in studying the structure and function of presents and produce function of the post translate the sequence of the post in the post of the p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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                                                                                                                                                                                                                                                                                                                                                                               Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which may be produced using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.1%; Score 2237.5; DB 3; 60.2%; Pred. No. 3e-130;
                                                                                                                                                                                                                                              Connolly K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Fig 39A-E; 260pp; English.
                                                                                                                                                                                                                                              Zhang G,
                                                                                99EP-00119184.
                                                                                                                                    98US-00169768.
                                                                                                                                                                                                                                              Buechter DD,
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                                                                                                                                                                                       (USSU ) US SURGICAL CORP
                                                                                                                                                                                                                                                                                               WPI; 2000-259138/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      medical implants.
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                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA12503
                                                                                07-OCT-1999;
                                                                                                                                    09-OCT-1998;
                                                                                                                                                                                                                                        Gruskin EA,
                         12-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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epoxyproline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bioadhesives), and for incorporating a wide variety of groups, including therapeutic ligands and biological probes, into polypeptides 8888888888

Sequence 1058 AA;

12; 510 558 357 108 417 168 477 300 657 341 717 393 777 453 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 897 898 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 957 ----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 48 GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPP GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 358 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGARGQA 418 GVMGFPGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAGGPGAGPGFAGPAGERGEQGPA ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 598 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----658 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPGPFGPIGNVGAPGAKGARGSAGPPGATGFP ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 64.1%; Score 2237.5; DB 3; Length 1058; 60.2%; Pred. No. 3e-130; ive 23; Mismatches 152; Indels 117; GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----Query Match
Best Local Similarity 60.2<sup>3</sup>
Matches 441; Conservative GDLGAPGPSGPAG GPPGPPGPPGPPG GPPGP-----1018 538 718 454 838 511 109 169 478 342 394 778 49 213 259 301 g рp  $\delta$ g 셤 ઠે a ò Db d 엄 d g d ò g ò ò ò ò à ò ò à ठ

RESULT 6 AAY84540 ID AAY84540 standard; protein; 1107 AA. (first entry) 25-JUL-2000 HX S X H

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; decorin; chimera. sequence of a chimeric collagen 1 (alphal)/decorin protein 858 /note= "Gly encoded by GCT" Location/Qualifiers 99EP-00119184 Key Misc-difference Homo sapiens. Unidentified. Chimeric. 07-OCT-1999; 09-OCT-1998; 12-APR-2000. EP992586-A2 acid Amino 

Production of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful medical implants. WPI; 2000-259138/23. N-PSDB; AAA12500.

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Zhang

EA, Buechter DD,

Gruskin

(USSU ) US SURGICAL CORP

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Claim 24; Fig 18; 260pp; English

The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by the cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acid, cellected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinagen and recombinant production of proteins such as collagen, fibrinagen and proteins depends on the post translational hydroxylation of protein protein also useful in studying the structure and functional protein sequence represente a chimment collagen 1 (alpha)/decorin protein, which may be produced using the method of the invention

Sequence 1107 AA;

356 416 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA Query Match 64.1%; Score 2237.5; DB 3; Length 1107; Best Local Similarity 60.2%; Pred. No. 3.1e-130; Matches 441; Conservative 23; Mismatches 152; Indels 117; 49 357 109

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| PR 09-OCT-1998; 98US-00169768.  XX X | The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by that cell for naturally occurring codons not preferred by that cell for naturally occurring codons not preferred by that cell for naturally occurring codons not preferred by that cell for naturally occurring codons not preferred by the cell.  C coll with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, cell with a hypertonic growth medium containing at least one amino acid, collito the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the cecombinant production of proteins such as collagen, fibrinogen and fibronectin whose ability to self aggregate and produce function of proteins depends on the post translational hydroxylation of proline. The present sequence represents climenic collagen 1 (alpha1)/transforming corporate translational trans-4-hydroxyproline. The present sequence represents climenic collagen 1 (alpha1)/transforming companies which of the invention.  XX Sequence 1171 AA; | a de se                       |
|---|---|---|
|   | Qy         301 GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGA 341           Db         657 GADGQPGAKGEPGAGKGPAGPPGPAGPPGPAGPRGARGSAGPPGATGFP 716           Cy         342  | 957 GPFGPPGSPGBGGPSGASGPAGPRGPGBGBGBGBGBGBGBGBGBGBGBGBGBGBGBGBGBG |

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fragment. The extracellular matrix protein is gating in a cell which does not ordinarily

The method comprises optimising a nucleic acid

In the cell by substitution of codons preferred trally occurring codons not preferred by the cell, really cocurring codons not preferred by the cell, leic acid sequence into the cell, and contacting the cyrowth medium containing at least one amino acid, promisting of trans-4-hydroxyproline and 3.

The consisting of trans-4-hydroxyproline and 3.

The consisting of trans-4-hydroxyproline and 3.

The acid as asimilate and incorporate trans-4-proteins. This is especially useful in the actions as samilate and incorporate trans-4-proteins. This is especially useful in the cottines such as collagen, fibringen and lifty to self aggregate and produce functional ne post translational hydroxylation of protein. The in studying the structure and function of from studying the structure and function of mormally contain trans-4-hydroxyproline. The seents chimetic collagen 1 (alphal)/transforming the sents chimetic collagen 1 (alphal)/transforming the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
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                                                                                                                                                                                                                                                                                                                                ar matrix proteins containing 4-trans-
native self aggregating proteins, useful on
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%; Pred. No. 3.3e-130;
23; Mismatches 152; Indels 117; Gaps
                                                                                                                                                Connolly K;
                                                                                                                                                Zhang G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
768.
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453
                                                                                       837 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV 896
                                                                                                             558
                                                                                                                                                         603
776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acid for expressing collagen or derivatives in plants - useful as, e.g. bio-materials and in therapeutic, cosmetic and odontological compositions.
                                                                                                                                                                                                                                                                                                                                                                        Primer, PCR, amplification; human; collagen; mammal; plant; prosthesis; cardiac valve; ligament; tendon; skin; gingival implant; perfumes; nerve regeneration; antibiotic; growth factor; cancer; inflammatory; gelatin; glue; food.
                                                                                                              GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                   GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEOGDRGIKGHRGFSGLO
                                                                                                                                                         GPPGP------AGPAGERGEOGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                      GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                     GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cleavage site for carboxypeptidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "cleavage site for aminopeptidase"
1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .22
/note= "signal peptide"
23. .999
/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                    AAW68485 standard; protein; 1464 AA
                                                                                                                                                                                                                                                                                                                                                      Human recombinant collagen protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-FR002331
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                                                                                                                                                                                                                             GPPGPPGPPG 1029
                                                                                                                                                                                                       GDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-362771/31.
N-PSDB; AAV60814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOC-) BIOCEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1996;
                                                                                                                                                                                                                                                                                                                                 08-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9827202-A1
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Bournat P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Peptide
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The invention relates to the production of mammalian collagen in plants. CC clones: alpha3 and alpha22, spanning the human collagen type I gene were isclated from a NG-63 osteosarcoma library. Clone alpha3 contained 53 by of the 5' untranslated region and the first 1920 by of coding consequence conceding amino acids are 2 clones were used to generate a number of fragments which were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (In) - 4 to 479; (B) containing cc fragments are: (A) containing nucleotides (In) - 4 to 479; (B) containing cc fragments are: (A) containing nucleotides (In) - 4 to 479; (B) containing cc fragments are: (A) containing nucleotides (In) - 4 to 479; (B) containing cc fragments of the sequence encoding the PRS (pathogenesis-related companies) of the sequence encoding the PRS (pathogenesis-related companies) of the central helicoidal and bases 66.77 from the sequence encoding the CC the amino propeptide domain (In 72-479); (D) all of the amino-telopeptide commin (In 474-534) and the N-terminus of the helicoidal region (In 535-cd and In) (E) the Draill Flammil fragment (1709-2808) of alpha22, encoding as 936-1192 in the central helicoidal domain creding as 1931-1444 in the C-propeptide domain; (G) the C-terminus of the C-terminus of the Cr propeptide domain; (G) the C-terminus of the C-terminus of the C-terminus of an al 193-1444 in the C-propeptide domain; (G) the C-terminus of the C-terminus of cencoding as 1343-1401 and also including the KDEL morif for retention in the ER. This sequence represents a recombinant thuman collagen; (F) and (G). Cr plant cells. The transformed plants; microcapsules for cardiac values, guide compositions (e.g. as prostheses for cardiac valves, ligaments of themostatic operation, adontological, cosmetic and bioechnological compositions (e.g. as prostheses for cardiac valves, ligaments of cuttered to collagen dystunction produced from the p 

Seguence 1464 AA;

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212 757 300 GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453 517 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGERGEQGPA 637 878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP GVMGFPGPXGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA GSPGFPGGLPGPAGPPGGAGKPGEQGVPGDLGAPGPSGPAGE------PGP----ĠŚPĠFQĠĽPĠPAĠPPĠĠAĠĸPĠĠQĠVPĠĎĽĠAPĠPŚĠARĠĖRGFPGERGVQGPPĠPAGPR --TGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSPGPAGPKGSP GE-----AGREGEAGLEGAK-----GLIGSEGSEGFDGKIGEEGEAGODGRE ĠĸŊĠŶŖĠĿſĠ₽ŀĠ₽ġĠŖġĠŖĠĠŖĸĠŖĸĠŖĸĠŖĠĠĸĠĸĠĸĠĠŖĠŖŶĠŖĸĠŖĸĠŖĸ ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GPPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA Gaps 64.1%; Score 2237.5; DB 2; Length 1464; 60.2%; Pred. No. 3.9e-130; ive 23; Mismatches 152; Indels 117; 441; Conservative Query Match Best Local Similarity 49 518 109 578 169 638 259 758 301 818 342 213 Matches

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                                                                      998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
                                                                                                                          1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDXGETGEQGDRGIKGHRGFSGLQ 1117
                                                                                                                                                                            GPHGPPGSPGEQGPSGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPV 1177
938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 997
                                           GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a composition comprising two or more isolated rate of human polymucleotides witch represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates subjected to pain, a method for identifying a differentially expression of a polymucleotide sequence which is differentially expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a
                                                                                                     ----AGAQ 558
                                                                                                                                                      GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                    chronic constriction injury; CCI;
                                                                                                  GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE
                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal tissue; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                           Human Protein P02452, SEQ ID NO 10491
                                                                                                                                                                                                                                                                                                         ADD45059 standard; protein; 1464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     segmental nerve injury; cl
nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English.
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26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                     1178 GPPGPPGPPGPPG 1190
                                                                                                                                                                                                            GDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-268312/26
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spinal segmer
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CXI) and spared nerve injury (CNII) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPG 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.1%; Score 2237.5; DB 7; 60.2%; Pred. No. 3.9e-130; ive 23; Mismatches 152;
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Best Local Similarity 60.23
Matches 441; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1464 AA;
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1178 GPPGPPGPPG 1190

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially respressed in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of an one of the polynucleotides the activity of one or more of the pain and a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more oppolypeptides or their antibodies. The polynucleotide or the compound that compound that is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form pair of the printed the specification) but was obtained in electronic form directly from WIPO at the contact of the printed for the printed for the contact of the printed for the contact of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                      Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Costigan M;
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                                                                                                                                                          Human Protein P02452, SEQ ID NO 10487
                   ADD45055 standard; protein; 1464 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                              (first entry)
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(FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-268312/26.
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                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                  ADD45055;
ADD45055
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64.1%; Score 2237.5; DB 7; Length 1464; 60.2%; Pred. No. 3.9e-130; ive 23; Mismatches 152; Indels 117; Best Local Similarity 60.2 Matches 441; Conservative Query Match

12;

Indels 117; Gaps

998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPP 1057 1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117 1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLMGLPGPIGPPGPRGRTGDAGPV 1177 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168 578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPA 637 ---TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 258 698 GANGAPGUDGAKGDAGAPGAPGSQGAPGLQGMPGBRGAAGLPGPKGDRGDAGPKGADGSP 757 GE----AGREGEAGLEGAK-----GLTGSEGSEGEDGKTGPEGEAGDGRE 300 ----VGPACKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453 454 GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPF 510 559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----511 GARGQAGVMGFPGFKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-----AGAQ ---GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 301 GPPGPPGARGO------AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----Human, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury, SNI, Chung. Human Protein P02452, SEQ ID NO 10483. ADD45051 standard; protein; 1464 AA. 1178 GPPGPPGPPGPPG 1190 604 GDLGAPGPSGPAG 616 (first entry) WO2003016475-A2 29-JAN-2004 Homo sapiens 27-FEB-2003 342 49 109 638 259 213 ADD45051; RESULT 11 Op g à 8 à 유 ò g ò ò 임 ò g ò ò 임 à CD g ð 8 à

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998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGPV 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine, alphal(I) collagen, gelatin, cytostatic, viral infection, barmaceutical, food industry, cosmetic, autoimmune disorder, vaccine, medical, arterial sealant; bone graft; dermal implant; haemostat; cancer, rheumatoid arthritis; beverage; photographic application.
                                                                                                                                                            818 GADGOPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
                                                                                                                                                                                                                                                                                                                                 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGPPGADGVAGPKGPAGERGSP 453
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                                                                                                                                                                                                                                                                      878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
-GLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                                                                                                                                                                                       ----VGPAGKDGEAGAQGPPGPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
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/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
ctggtcccccggccctgctgga"
                                                  758 GKDGVRGLTGPIGPPGPAGAPGDKGBSGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP
                                                                                                             301 GPPGPPGARGO------AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
                                                                                                                                                                                                                                                                                                                                                                                          938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                            GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 GARGQAGVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seeley TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02535 standard; protein; 1449 AA.
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GE-----AGRPGEAGLPGAK--
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10-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic design a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the paint and a pharmaceutical composition and a pharmaceutical composition of a pharmaceutical composition, a method for identifying a compound useful in the activity in an animal of one or more of the polypeptides given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence acts of the securing pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                        Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                     Befort K,
                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
  14-AUG-2002; 2002WO-US025765
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Best Local Similarity 60.23
Matches 441; Conservative
                                                                                                                                                                  (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
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The present sequence is porcine alphal(I) collagen. The present invention relates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is useful in medical, pharmaceutical, food and cosmetic industries. Collagen is useful in medical, pharmaceutical, food and cosmetic incontinence implants, and for treating autoimmune disorders such as submitted arthritis. Collagen is useful in food products such as sausage casings, and in cosmetics or facial and skin products such as sausage animatoid arthritis. Collagen is useful in food products such as sausage casings, and in cosmetics or facial and skin products such as monitaring viral infections, autoimmune diseases and cancer. Gelatin is useful in the manufacture or as a component of various pharmaceutical and medical devices and products, in food and beevrage industries, in hair manufacturing processes, as a glue or adhesive in various manufacturing and photographic application; in laboratory application, and as a component in various gels used for biochemical and electrophoretic analysis, including enzymographic gels
  and for treating autoimmune disorders, infections and cancer.
                                                       Example 3; Fig 8; 168pp; English.
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Sequence 1449 AA;

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                                                                                                      GARGEPGPAGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                         GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
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                                  Indels 94; Gaps
   Length 1449;
 64.0%; Score 2234; DB 4; 162.0%; Pred. No. 6.4e-130; ive 21; Mismatches 154;
Query Match
Best Local Similarity 62.0%
Matches 438; Conservative
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New pancreatic specific nucleic acid molecule or protein for diagnosing, staging, imaging, monitoring, preventing or treating pancreatic cancer or non-cancerous disease states of the pancreas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGFRGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- PGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.0%; Score 2233.5; DB 7; Length 1161; 60.0%; Pred. No. 5.7e-130; ive 23; Mismatches 153; Indels 117;
                                                                                                                                                                                                                                                                    cell; pancreatic cancer;
                  573 QGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-
                                                                                                                                                                                                                                Human pancreatic cell protein sequence SegID510.
                                                                                                                                                                                                                                                                                   cancer death; cytostatic; vaccine; gene therapy
non-cancerous pancreas disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; SEQ ID NO 510; 635pp; English
                                                                                                                                                                                                                                                                    cell; pancreatic
                                                                                                                       ΑĀ
                                                                                                                     ADE87050 standard; protein; 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2002; 2002WO-US040655.
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                                                                                                                                                                                                                                                                    pancreatic
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N-PSDB; ADE87387.
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Best Local Similarity
Matches 440; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1161 AA;
                                                                                                                                                                                                                                                                                                                                                                          WO2003060145-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                    neoplastic
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                                                                                                      ADE87050
                                                                                     RESULT
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                                   GE----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                                                      575 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                                                                                                               635 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                                                                                                                                                                                                                                                                        GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                       ---AGAQ
                                                                                                                                                                                                                                                                                                                                               GPAGKSGDRGETGPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ
                                                                                                                                             GADGOPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP
                                                                                                                                                                       ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                      GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                                                                                                      GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
                        -TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                        GPPGPPGARGO-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, deer, rat, mouse, DACC, deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocyte; chondrogenesis; osteogenesis; growth; repair; regeneration; restoration; extracellular matrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist;
                                                                                                                                                                                                                                                                                                                       GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide orthologous to DACC-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG93947 standard; protein; 1461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonist; gene therapy.
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The invention discloses a method for stimulating or inhibiting cell growth and/or division which comprises contacting or inserting into an animal cell a polypeptide comprising one of the dear antler cartilage cell (DACC) clones disclosed. More particularly, the method relates to these polypeptides capable of stimulating mesenchymal cell growth and/or division and to transferding these cells and chondrocytes with vectors carrying the genes of these polypeptides capable of stimulating chondrogenesis, osteogenesis, growth, repair, regeneration and/or restoration of the extracollular matrix. The chondrocytes selectively express genes required to form a cartilaginous matrix. The Cholypeptides and polynclectides are useful for identifying an agent that modilates the activity of the polypeptide, for stimulating mesenchymal cell growth and/or division by exposing animal mesenchymal cells to conditioned media or its active fraction, obtained from dear antler cartilage cells, for inhibiting cell growth and/or division by inserting into an animal cell, a compound which inhibits the translation of the polywoleotide encoding the DACC. The method and the polypeptides are useful for stimulating mesenchymal cell cor connective tissue growth, repair, regeneration and/or restoration in an animal. The polymucleotides, polypeptides, agonists and antagonists car animal. The polymucleotides, polypeptides, agonists and antagonists collectify other proteins, which bind to or interact with the polymored in modulating cell growth and/or division.

The sequences presented in ABG93921-ABG99948 are the proteins encoded by the DACC CDNA clones 514 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108 575 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634 754 Stimulating or inhibiting cell growth and/or division, useful for stimulating chondrogenesis, cartilage, disc or connective tissue growth, repair, and/or regeneration, comprises administering deer antler |||| GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 515 GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP---GSPGFPGGLPGPPGBAGKPGBQGVPGDLGAPGPSGARGBRGFPGBRGVQGPPGPAGPR -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 1 GPP------GEPGPIGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA Length 1461; Indels 64.0%; Score 2233.5; DB 5; 153; Pred. No. 6.9e-130; ; Mismatches 153; Claim 13; Page 154-160; 214pp; English. 64. 60.08; Fr. 23; 440; Conservative Similarity Sequence 1461 AA; cartilage gene Query Match Best Local S: Matches 440 455 49 695 109 169 635 213 259 ठे 염  $\delta$ a ò 음  $\dot{\delta}$ g  $\delta$ 셤 δ

755 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPP 814 ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 GADGQPGAKGEPGDAGARGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP GAAGRVGPPGPSGNAGPPGPPGPPGKBGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP ---AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----GPPGPPGARGQ----301 815 342 875 임 ठ g à 셤

> L5-FEB-2002; 2002WO-AU000163 15-FEB-2001; 2001AU-00003116

(ADPP-) ADP PHARM PTY (UNSY ) UNIV SYDNEY.

WPI; 2002-643456/69

Ghosh P;

Roubin R,

394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453

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1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulatory; cytostatic; neuroprotective; vulnezary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporossis; tissue regeneration; immune disorder.
GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                      GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAP
                                                                                                                                                                                                                                                                                                          1055 GPAGKSGDRGETGPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ
                                                                                                                                                                                                                                                                                                                                                                                 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                             GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU14136 standard; protein; 1464 AA.
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998 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                         517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             698 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                         458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VGPAGKDGEAGAQGPPGPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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23;
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completed: October 18, 2004, 13:37:26

Search

GPPGPPGPPGPPG

001 (0. 11. 10. 1) Date

Job time : 104.398 secs

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RESULT 1
US-09-331-347C-21
                                                                                                                                           October 18, 2004, 13:31:20 , Search time 24.4569 Seconds (without alignments) 1673.075 Million cell updates/sec
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                                                                                                                                                                                                                                                US-10-658-989A-2
3488
1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 617
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                 478139 segs, 66318000 residues
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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# SUMMARIES

|           |                       |                     | _                |                  |                  | _                |                   | _                 | _                 | _                | _                |                   |                  |                 | _                | _                |                  |                  |                   |                  |                  | _                |                 |       |                  | _                | _                | _                 |
|-----------|-----------------------|---------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|-----------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|-----------------|-------|------------------|------------------|------------------|-------------------|
|           |                       |                     |                  |                  |                  |                  |                   |                   |                   |                  |                  |                   |                  |                 |                  |                  |                  |                  |                   | `                |                  |                  |                 |       |                  |                  |                  |                   |
|           | Description           |                     |                  | 18,              | 18,              |                  | Sequence 9, Appli | Sequence 9, Appli | Sequence 1, Appli | 4                | 10               | Sequence 3, Appli | 20               | ř               | 20               | 20               | 20,              | 12,              | 12,               | 48,              | 50,              | 62               | 4,              | 4,    |                  | 21               | 21               | Sequence 21, Appl |
| SUMMAKIES | ID                    | US-09-331-347C-21   | US-08-963-825-18 | US-09-500-811-18 | US-09-570-573-18 | US-09-548-608-18 | US-09-585-887-9   | US-09-289-578-9   | US-08-931-820-1   | US-09-219-849-49 | US-08-468-996-10 | US-08-931-820-3   | US-08-963-825-20 | US-09-010-999-1 | US-09-500-811-20 | US-09-570-573-20 | US-09-548-608-20 | US-08-316-650-12 | PCT-US95-02251-12 | US-09-219-849-48 | US-09-219-849-50 | US-08-642-255-62 | US-08-931-820-4 | o     | US-08-642-255-53 | US-08-963-825-21 | US-09-500-811-21 | US-09-570-573-21  |
|           | Length DB             | 1464 4              | 1341 3           | 1341 3           | 1341 3           | 1341 3           | 1461 4            | 1461 4            | 1057 3            | 822 3            | 1017 4           | 1060 3            | 1418 3           | 1418 3          | 1418 3           | 1418 3           | 1418 3           | 1442 2           | 1442 5            | 595 3            | 595 3            | 1064 1           | 1057 3          | 720 3 | 777 1            | 1078 3           | 1078 3           | 1078 3            |
| e)¢°      | Query<br>Match Length | 64.1                | 63.9             | 63.9             | 63.9             | 63.9             | 63.8              | 63.8              | 63.3              | 62.8             | 56.0             | 55.7              | 55.7             | 55.7            | 55.7             | 55.7             | 55.7             | 55.5             | 55.5              | 54.0             | 54.0             | 54.0             | 53.1            | 52.7  | 52.7             | 52.6             | 52.6             | 52.6              |
|           | Score                 | 2237.5              | 2228.5           | 2228.5           | 2228.5           | 2228.5           | 2224.5            | 2224.5            | 2208.5            |                  | 1955             | 1943              | 1943             | 1943            | 1943             | 1943             | 1943             | 1936             | 1936              | 1882.5           | 1882.5           | 1882.5           | 1853            | 1837  | 1837             | 1833.5           | 1833.5           | 1833.5            |
|           | Result<br>No.         | 1 rd<br>1<br>1<br>1 | 7                | ო                | 4                | ß                | 9                 | 7                 | 00                | σ                | 10               | 11                | 12               | 13              | 14               | 15               | 16               | 17               | 18                | 19               | 20               | 21               | 22              | 23    | 24               | 25               | 26               | 27                |

| Sequence 21, Appl | Sequence 2, Appli | Seguence 19, Appl |                  | Sequence 19, Appl | Seguence 19, Appl | Sequence 10, Appl | Sequence 10, Appl | Sequence 72, Appl | Sequence 5, Appli | Sequence 12, Appl | Sequence 56, Appl | Sequence 132, App |                   |                  | Sequence 103, App  |                   | Sequence 75, Appl |
|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|--------------------|-------------------|-------------------|
| US-09-548-608-21  | US-08-931-820-2   | US-08-963-825-19  | US-09-500-811-19 | US-09-570-573-19  | US-09-548-608-19  | US-09-585-887-10  | US-09-289-578-10  | US-08-642-255-72  | US-09-219-849-5   | US-08-468-996-12  | US-09-919-497-56  | US-08-642-255-132 | US-08-397-633A-53 | US-08-175-155-68 | US-08-477-509B-103 | US-08-642-255-101 | US-08-707-237A-75 |
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| 1078              | 1024              | 1366              | 1366             | 1366              | 1366              | 1366              | 1366              | 1065              | 960               | 492               | 1806              | 829               | 829               | 837              | 837                | 837               | 837               |
| 52.6              | 50.6              | 50.6              | 50.6             | 50.6              | 50.6              | 50.5              | 50.5              | 48.7              | 48.0              | 47.2              | 47.1              | 46.4              | 46.4              | 46.4             | 46.4               | 46.4              | 46.4              |
| 1833.5            | 1764              | 1764              | 1764             | 1764              | 1764              | 1762              | 1762              | 1699.5            | 1674              | 1645              | 1644              | 1619.5            | 1619.5            | 1619.5           | 1619.5             | 1619.5            | 1619.5            |
| œ                 | 6                 | 0                 | $\vdash$         | N                 | m                 | 4                 | 35                | 9                 | 7                 | 80                | σ                 | 0                 | Н                 | N                | m                  | 4                 | īŪ                |

# ALIGNMENTS

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                                                                                                      Length 1341;
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A Method for Assaying Collagen Fragments

in Body Fluids, A Test Kit and Means for

method and Use of the Method to Diagnose

Disorders Associated with the Metabolism
                                                                                                   63.9%; Score 2228.5; DB 3; Length 60.0%; Pred. No. 4.2e-133; ive 23; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE----
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Fatent No. 6223314
GENERAL INFORMATION:
APPLICANT: Worlst, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for As
TITLE OF INVENTION: in Body Fluids,
                                          (1)
                 IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1
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    Homo sapiens
                                                                                                                                                440; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out tITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCES: 21
                                                                                                                                                                                                                                       1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
                                                                                                                                                                                                                                                                                                                                                                                                                  1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
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                                                                           GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
                                                                                                                       394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                                                                              GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 877
                                                                                                                                                                                                          GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                       -----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                             938 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP
                                                                                                                                                                                                                                                                                          511 GARGQAGVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGEN INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-527-770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-963-825-18
Sequence 18, Application US/08963825
Patent No. 6110689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTA.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                616
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 GDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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Sequence 18, Application US/09570573

Fatent No. 6442361

GENERAL INFORMATION:
APPLICANT: GVISt, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments for Carrying Out the TITLE OF INVENTION: Abody Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                         559 GPPGP-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                 GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                                                                                                                                                                                                                      GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 GDLGAPGPSGPAG
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US-09-570-573-18
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NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
COTNTRY: USA
ZIP: 10022
COMPUTER: ENABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Versior
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
APPLICATION NUMBER: 08/187,319
FILING DATE:
APPLICATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 212-527-7700
TELEPAX: 212-53-6237
TELEPAX: 212-73-6237
TELEPAX: 236-73-6237
                                                                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: COLLAGEN ALPHA 1 (I)
US-09-500-811-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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GY: linear
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COUNTRY: NEW ACCEDED TO THE NEW 
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CLONE: COLLAGEN ALPHA 1
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GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168

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342

GPPGPPGARGO-----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA--- 341

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393

GE-----AGREGEAGLEGAK-----GLIGSEGSEGEDGKIGEEGEAGQDGRE 300

213 ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP

514 GSPGFPGGLPGPAGPPGEAGKPGEPGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 573

169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP----

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Indels 117; Gaps

GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108 

GPP------GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA

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GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4305/08701
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET 1905
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-52-7700
TELERA: 216-87-7700
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
: 805 Third Avenue
New York
New York
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                                                                                                                   ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
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                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                   SOFTWARE:
                                                         STATE: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POPOLOGY:
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Matches 440;
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Db
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Sequence 18, Application US/09548608

Patent No. 6355422

GENERAL INFORMATION:
GENERAL Sende, Martin

APPLICANT: Goide, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             994 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGP1GPPGPRGRTGDAGPV 1053
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                                                                                                                                                                                                                              334 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 393
                                                                                                                                                                                                                                                                                        GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                                                                                                                                                                                         GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA. 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE-----PGP---- 212
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                                                                                                                                                                          -GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            754 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPPGPAGEKGSP
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                                                                                                                       Gaps
                                                             Length 1341;
                                                                                                                Indels 117;
                                                                DB 3;
                                                         tch 63.9%; Score 2228.5; DB 3; al Similarity 60.0%; Pred. No. 4.2e-133; 440; Conservative 23; Mismatches 153;
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                                                      Query Match
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| CY   259 GEAGRPGBAGLPGAKGLTGSPGSPGRPDGKTGPPGPAGQDGRP 300   | Qy         342VGPAGKDGEAGROGPPGPAGPAGERGEOGPAGSPGROGLEGPAGPPGEACKP 393           Db         975 GAAGRVGPPGPSGNAGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGEKGSP 934           Qy         394 GEQGVPGDLGAPGPPGEPGPTGLPGPPGERGGPRGERGFPGADGVAGPKGPAGERGSP 453           Db         935 GADGPAGAPGTPGPPGILPGPPGERGPPGLPGPSGEPGRAGERGSP 994       | 4 6 7<br>10 0 1 |  | SULT 7 -09-289-578-9 Sequence 9, Application US/0 Bartent No. 6428978 GENERAL INFORMATION: APPLICANT: Olsen, David R APPLICANT: Chang, Robert APPLICANT: Chang, Robert APPLICANT: Chang, Robert APPLICANT: Chisholm, Hugh APPLICANT: Chisholm, Georg TITLE OF INVENTION: FULL-ITTLE OF INVENTION: CHILL FITTLE OF INVENTION: CELLS FILE REFERENCE: 22500203040 CURRENT APPLICATION UMBER:   | CORRENT FILING DATE: 1999-04-10   |
|--|--|-----------------|--|---|---|
| Qy       394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453         Db       814 GADGPAGAPGTPGPGAIAGQRGVVGLPGQRGERGFPGLPGPSGEPGRGPSGASGERGPP 873         Cy       454 GPAGPKGSPGBAGRPGPAGAPGTBAGALPGARGTPGPPGPAGQDGRRGPPGPP 510         Db       874 GPMGPPGLAGPPGESGREGAPGAPGAPGASGARGARGARGARGARGARGARGAPGPV 933 | QY         511 GARGQAGVMGFPGPKGAAGERGVPGBPGAVGPAGKDGEAGAQ 558           Db         934 GPAGKSGDRGETGPAGPAGPAGARGPAGPRGPRGERGEGGDRGIKGHRGFSGLQ 993           QY         559 GPPGPAGPAGERGEGGPRGBAGSPGFQGLPGPAGPPGEACKPGEQCVP 603           Db         994 GPPGPPGSPGERGGPGGPRGSPGSAGAPKGPPGSAGAPKGPPGEACKDGLAGPPGFRGFRGAGTGDAGPV 1053 | 604<br>1054     | RESULT 6  US-09-585-887-9  Sequence 9, Application US/09585887  Patent No. 6413742  GENERAL INFORMATION  APPLICANT: Olsen, David R  APPLICANT: Chang, Robert  APPLICANT: Hitzenan, Ronald A.  APPLICANT: Hitzenan, Ronald A.  APPLICANT: Hitzenan, Ronald A. | TITLE OF INVENTION: OUTLING, WELL TITLE OF INVENTION: PULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT TITLE OF INVENTION: CELLS. FILE REFERENCE: 225002030400 CURRENT FILING DATE: 2000-05-31 CURRENT APPLICATION NUMBER: US/09/585,887 CURRENT PLING DATE: 1999-04-09 PRIOR FILING DATE: 1999-04-09 PRIOR FILING DATE: 1999-06-08 NUMBER OF SEQ ID NOS: 11 SSEQ ID NO 9 LENGTH: 1461 TYPE: PRT CREATION OF SEQ ID NOS: 11 CONGANISM: Homo sapiens US-09-585-887-9 | Query Match         63.8%;         Score 2224.5;         DB 4;         Length 1461;           Best Local Similarity         59.9%;         Pred. No. 8e-133;         Indels 117;         Gaps         12;           Matches         439;         Conservative         23;         Mismatches         154;         Indels 117;         Gaps         12;           Qy         455         GPPGGPGGEGGRGGPGGRGGPGGRGGPGGRGGPGGAGGRGGPGAGGRGGPGAGGAGGGGGAGGGGGAGGGGGGGG |

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                                                                                                                                                                                                                                                                                                                                                                   GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                           429 GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 GPPGEAGKPGEOGVPGDLGAPGPSGARGERGFPGERGVOGPPGPAGPRGANGAPGNDGAK 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 GDAGAPGAPGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPI 608
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                                                                                                                                                                                                                             309 GPNGEAGSAGPPGPPGLRGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
                                                                                                                                                                                                                                                                           GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
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                                                                                                                                          105;
                                                                                               Length 1057;
                                                                                                                                          Indels
                                                                                          63.3%; Score 2208.5; DB 3; 60.3%; Pred. No. 6.2e-132; live 23; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/09219849; Patent No. 6150081; GENERAL INFORMATION: APPLICANT: VAN HEARD, GEORGE V. APPLICANT: VAN RIAN, ALEXIS C. APPLICANT: BOUWGTRA, JAN B. APPLICANT: DE WOLF, FREDERIK A. APPLICANT: WOOBROEK, ANDREAS; APPLICANT: WERTEN, WARC W.T.; APPLICANT: WIND, RICHELE D.
       Homo sapiens
3: Collagen type
                                                                                            Query Match 63.3
Best Local Similarity 60.3
Matches 435; Conservative
    ; ORGANISM: Hor;
; TISSUE TYPE:
US-08-931-820-1
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US-09-219-849-49
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GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 634
                                                                                                                                                                                                                                                                                                                   GPPGPPGARGQ-----34VMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         934
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                                                                                     GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR
                                                                                                                                     ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                                                                                GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      875 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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OUMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (E
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
                                             GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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US-08-931-820-1
; Sequence 1, Application US/08931820
; Patent No. 6010863
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1175 GPPGPPGPPG 1187
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RDNESS: single
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKTGPPGPAGQDGRPGPAGPPGARGQAGVMGFPGPKGTAGEPGKAGERGLPGPPGAVGPA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AGVMGFP 522
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                                                                                                                                                                                                                                                                                                                                                                                 48
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
TOUR SERVENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT PILLING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SERVENCE: ACCOUNTY OF 49
ILENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GPKGSPGEAGRP-----GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
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                                                                                                                                                                                                                                                                                                                                                                                 1 GPPGEPGPTGLPGPPGE------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                  Score 2191; DB 3; Length 822;
Pred. No. 6.3e-131;
2; Mismatches 158; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEOGRAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 616
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                                                                                                                                                                                                                                                                                                                  Query Match 62.8%; Soc
Best Local Similarity 56.9%; Pro
Matches 436; Conservative 22;
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                          ; OTHER INFORM
US-09-219-849-49
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ORAL ADMINISTRATION
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56.0%; Score 1955; DB 4;
Best Local Similarity 52.5%; Pred. No. 5.4e-116;
Matches 396; Conservative 38; Mismatches 182;
                                                                                                                                                                                                                                                                        TYPE
OSCUELLOW APPLICATION US/08468996
PACHEL NO. 6645504
GENERAL INFORMATION:
APPLICANT: Wainer, Howard
APPLICANT: Wainer, Howard
APPLICANT: Ariel
APPLICANTON: GUUCAGON
FILE OF INVENTION: GUUCAGON
FILE REFERENCE: 1010/16959-US3
CURRENT APPLICATION NUMBER: US 07/460,995
CURRENT FILING DATE: 1990-0-2.2
PRIOR FILING DATE: 1990-0-2.2
PRIOR PILING DATE: 1990-10-15
PRIOR PLING DATE: 1990-10-15
PRIOR PLING DATE: 1990-10-15
PRIOR PLING DATE: 1990-0-2.1
PRIOR PLING DATE: 1990-0-2.1
PRIOR PLING DATE: 1990-0-2.1
PRIOR PLING DATE: 1990-0-2.1
PRIOR PLING DATE: 1990-0-10-15
PRIOR PLING DATE: 1990-0-10-15
PRIOR PLING DATE: 1990-0-10
PRIOR PLING DATE: 1990-0-14
PRIOR PLING DATE: 1990-0-14
PRIOR PLING DATE: 1990-0-14
PRIOR PLING DATE: 1990-0-14
PRIOR PLING DATE: 1990-10-11
PRIOR PLING DATE: 1990-10-11
PRIOR PLING DATE: 1990-10-11
PRIOR PLING DATE: 1990-10-11
PRIOR PLING DATE: 1990-10-13
PRIOR PLING DATE: 1990-10-13
PRIOR PLING DATE: 1990-10-13
PRIOR PLING DATE: 1990-10-13
PRIOR PLING DATE: 1990-10-14
PRIOR PLING DATE: 1990-10-13
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US-08-468-996-10
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Sequence 20, Application US/08963825

Sequence 20, Application US/08963825

Parent No. 6110689

GENERAL INFORMATION:

APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
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                                                          GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 223
                                                                                                                 -----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                                                                                                                                                   224 GASGNPGTDG1PGAKGSAGAPG1AGAPGFPGPRGPPDPQGATGPLGPKGQTGKPG1AGFK 283
                                                                                                                                                                                                                          GD---LGAPGPSGPAGEPGPTGLP------GPPGERGGPGSRGFPGADGVA 237
                                                                                                                                                                                                                                                                         284 GEOGPKGEPGPAGPOGAPGPAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGQDGLA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
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                                                                                                                                                                                                                                                                                                                                                                    ------PGPTGLP-----GPPGBRGGPGSRGFPGADGVAGPKGPA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
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     GQDGRPGPPGPPGARGQAGVMGFP-
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CLASSIFICATION: 436
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US-08-963-825-20
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                                                                                    GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
                                                                                                                    445 GPAGPAGERGEQGAPGPSGFQGLPGPPGBAGKPGDQGVPGEAGAPGLVGPRGERGFP 504
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GRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPP
                                                                                                                                                                                          -----GPPGERGGPGSRGFPGADGVAGPKGPA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
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APPLICATION NUMBER: US/08/931,820 FILING DATE:
                                                                                                                                                                                                                                                                                                         GERGSPGPAGPKGSPGE------
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US-08-931-820-3
F. Sequence 3, Application US/08931820
; Patent No. 6010863
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: Collagen type II
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
TYPE: amino acid
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Matches 393; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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) TISSUE TYPE:
US-08-931-820-3
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816 GARGAQGPPGATGFPGAAGRVGPPGSNGNPGPPGPPGPSGKDGPKGARGDSGPPGRAGEP 875
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APPLICANT: Poole, Anthony P.
APPLICANT: Hollander, Anthony P.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billinghurst, R. C.
APPLICANT: Billinghurst, R. C.
APPLICANT: Billinghurst, R. C.
APPLICANT: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Score 1943; DB 3; Length 1418;
52.1%; Pred. No. 4e-115;
iive 34; Mismatches 189; Indels 138;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

TLING DATE:

APPLICATION NUMBER:

CLASSIFICATION:

4335

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

BRICK APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

TOTUL 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

TILING DATE:

APPLICATION NUMBER:

TILING DATE:

APPLICATION NUMBER:

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APPLICATION NUMBER:

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NAME:

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COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-010-999-1
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US-09-010-999-1
Sequence 1, Application US/09010999
Patent No. 6132976
; GENERAL INFORMATION:
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TELECOMMUNICATION (202) 672-5300
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.1%
Matches 393; Conservative
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STRANDEDNESS:
TOPOLOGY: 1:--
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STREET: 3000
TTY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 GDRGDVGEKGPEGAPGKDGGRGLTGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGER 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 GNDGQPGPAGPPGPVGPAGGPGPPGARGBAGPTGARGPBGAQGPRGEPGTPGSPGPA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 gasgnpgrogipdakgsagapgiadapgepeppeppopopigargplopkgorgkpgiadfk 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
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55.7%; Score 1943; DB 3; Length 1418;
Best Local Similarity 52.1%; Pred. No. 4e-115;
Matches 393; Conservative .34; Mismatches 189; Indels 138;
          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHONE: 212-527-7700
TELECHONE: 212-527-7700
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INMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                 TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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TOPOLOGY:
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US-08-963-825-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGFPGPPDPQGATGPLGPKGQTGKPGIAGFK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GEQGPKGEPGPAGPQGAPGPAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGQDGLA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 GPAGPAGERGEQGAPGPSGFQGLPGPPGPPGEGGKPGDQGVPGEAGAPGLVGPRGERGFP 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sa6 gergspgaoglogbrdlpgtpgtdgpxgasgpagbpgaogbpglogmpgergaagiagbk 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                    55.7%; Score 1943; DB 3; Length 1418; 52.1%; Pred. No. 4e-115; ive 34; Mismatches 189; Indels 138;
                                       NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-527-7700
TELEFAX: 212-753-6237
TELEFAX: 23687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                ORIGINO...
ORGANISM: Homo ...
INMEDIATE SOURCE:
"TONE: COLLAGEN -ALPHA 1 (11)
    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.1
Matches 393; Conservative
                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                      amino acid
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MOLECULE TYPE:
ORIGINAL SOURCE:
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GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 335
                                           -----GKDGEAGAQGPPGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                                                       336 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 395
                                                                                                                                                                 396 GEQGPKGEPGPAGPQGAPGPAGEEGKRGARGEPGGVGPIGPPGERGAPGNRGFPGQDGLA 455
                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                                    575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483
                                                                                                                            -GPPGERGGPGSRGFPGADGVA 237
                                                                                                                                                                                                                                                                                           GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09500811
Patent NO. 61231314
GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for
TITLE OF INVENTION: Method and Use of the Method to Diagnose of TITLE OF INVENTION: Disorders Associated with the Metabolism on NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616
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APPLICATION NUMBER: US/09/500, FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
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ADDRESSEE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
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US-09-500-811-20
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336 GASGNPGTDGIPGAXGSAGAPGIAGAPFPGPRGPPDPQGAIGPLGPXGQTGKPGIAGFK 395
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                                                                                                                                      GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
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                                                             GD---LGAPGPSGPAGEPGPTGLP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.7%; Score 1943; DB 3;
52.1%; Pred. No. 4e-115;
tive 34; Mismatches 189;
                                GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                                                                                                                                                                                              STREET: Darby & Darby PC STREET: 805 Third Avenue CITY: New York COUNTRY: USA ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      Sequence 20, Application US/09570573
Patent No. 6342361
GENERAL INFORMATION:
APPLICANT: QYIEt, Per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REPREBNCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 236687
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 amino acids
                                                                                                                                                                                               APPLICANT: OVISE, PER APPLICANT: BONGE, MAITIN TITLE OF INVENTION: A Method TITLE OF INVENTION: Method TITLE OF INVENTION: Disord NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: Darby & Darby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.1
Matches 393; Conservative
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GY: linear
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TOPOLOGY:
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US-09-570-573-20
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

146 OCL 19 09:2/.38 200

October 18, 2004, 13:42:06 ; Search time 79.3776 Seconds (without alignments) 2513.149 Million cell updates/sec 3488 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 617 1360919 segs, 323318874 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-658-989A-2 Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications AA:\*

1: /cgn2\_6/ptodate/2/pubpaa/USO7\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodate/2/pubpaa/USO7\_PUBCOMB.pep:\*
3: /cgn2\_6/ptodate/2/pubpaa/USO6\_NEW\_PUB.pep:\*
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8: /cgn2\_6/ptodate/2/pubpaa/USO8\_PUBCOMB.pep:\*
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19: /cgn2\_6/ptodate/2/pubpaa/USO0\_PUBCOMB.pep:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description         | Sequence 20, Appl | Sequence 11, Appl | Sequence 8, Appli | 10,              | Sequence 21, Appl | Sequence 1, Appli |                 | Sequence 150, App | ω               | Sequence 8, Appli | 4                | Sequence 243, App |                  | Sequence 18, Appl |
|---------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-----------------|-------------------|-----------------|-------------------|------------------|-------------------|------------------|-------------------|
| QI                  | US-10-104-889-20  | US-10-104-889-11  | US-10-104-889-8   | US-10-104-889-10 | US-10-216-705-21  | US-10-357-851-1   | US-10-358-024-1 | US-10-788-792-150 | US-10-402-089-8 | US-10-402-072A-8  | US-10-468-091-25 | US-10-291-265-243 | US-10-104-889-16 | US-10-058-124-18  |
| DB                  | 151               | 15                | 15                | 15               | 14                | 16                | 16              | 17                | 15              | 15                | 16               | 14                | 15               | 14                |
| Length DB           | 1057              | 1107              | 1171              | 1388             | 1464              | 1464              | 1464            | 1464              | 1449            | 1449              | 1461             | 1464              | 1057             | 1341              |
| %<br>Query<br>Match | 64.1              | 64.1              | 64.1              | 64.1             | 64.1              | 64.1              | 64.1            | 64.1              | 64.0            | 64.0              | 64.0             | 64.0              | 64.0             | 63.9              |
| Score               | 2237.5            | 2237.5            | 2237.5            | 2237.5           | 2237.5            | 2237.5            | 2237.5          | 2237.5            | 2234            | 2234              | 2233.5           | 2233.5            | 2231.5           | 2228.5            |
| Result<br>No.       | 1                 | 7                 | m                 | 4                | Ŋ                 | 9                 | 7               | œ                 | 6               | 10                | 11               | 12                | 13               | 14                |

| equence 263<br>equence 156<br>equence 36<br>equence 2,<br>equence 65                        | oon  | equence 26<br>equence 49<br>equence 10<br>equence 1,                                    | equence 5 equence 6 equence 6 equence 6 equence 4 equence 4  | 2 2 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                      | equence 4,<br>equence 6,<br>equence 4,<br>equence 6,  |
|---|--|---|--|--|---|
| US-09-918-715-2<br>US-10-060-036-1<br>US-10-171-311-3<br>US-10-149-352-2<br>US-10-177-293-6 | US-10-301-822-<br>US-10-734-564-<br>US-10-402-089-<br>US-10-402-072A | US-10-468-091-<br>US-10-342-331-<br>US-10-639-286-<br>US-10-194-441A-<br>US-10-058-124- | US 10-468-091-5<br>US 10-194-441A-<br>US 10-468-091-6<br>US 10-233-885-4<br>US 10-231-581-4<br>US 10-326-508A- | US-10-232-17<br>US-10-232-17<br>US-10-342-33<br>US-10-342-03<br>US-10-402-08 | US-10-402-089-4<br>US-10-402-089-6<br>US-10-402-089-6<br>US-10-402-072A-4<br>US-10-402-072A-6 |
| 44444   | 464444   | 8222 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1  | 1418 14<br>10014 14<br>1487 16<br>714 14<br>714 14   | 2002<br>2002<br>2002<br>2003<br>2003<br>2003<br>2003                         | 7777<br>2000<br>2000<br>2000  |
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## ALIGNMENTS

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RESULT 1
US-10-104-889-20
Sequence 20, Application US/10104889
Sequence 20, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
BROKEN, DOUGLAS
BROKEN, DOUGLAS
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSE:
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STREET: NI SARLE OVINGTON BOULEVARD
CITY: NI ON SARLE OVINGTON BOULEVARD
CITY: NI ON SARLE OVINGTON BOULEVARD
COMMANDENCES OF SARLE OVINGTON BOULEVARD
CITY: NI ON SARLE OVINGTON BOULEVARD
COMMANDENCES OF SARLE OVINGTON BOULEVARD
CITY: NI ON SARLE OVINGTON BOULEVARD
COMMANDENCES OF SARLE OF
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ZIP: 11553
COMPUTER READABLE
FOORM: GISK
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BRIESES #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-Mar-2002
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFRAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 228-8
INFORMATION FOR SEQ ID NO: 20
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                                                                                                                                                                                                                                                           49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
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                                                                                                                                                                        Gaps
                                                                                                                                         DB 15; Length 1057;
                                                                                                                                                                    152; Indels 117;
                                                                                                                                      Query Match
64.1%; Score 2237.5; DB 19
Best Local Similarity 60.2%; Pred. No. 1.9e-104;
Matches 441; Conservative 23; Mismatches 152;
                                                           TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Sequence 11, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS

RESULT 2 US-10-104-889-11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

Guery Match

Best Local Similarity 60.2%; Pred. No. 2e-104;

Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---
                                                                                                                                     ADDRESSE: DILWORTH & BARRESE
STREET: 333 BARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                    COUNTRY: U.S.A.

ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Ver
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY, AGENT INFORMATION:
NAME: STEEN, JEPPREY S
TELECOMMUNICATION:
NAME: STEEN, JEPPREY S
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
)
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-104-889-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 228-8484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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daDGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP 716 GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGAPGPV 896 417 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPACKDGEAGAQGPPGPAGPAGERGEQGPA 476 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108 357 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA 416 597 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPP 777 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE 301 GPPGPPGARGQ-----GPPGP-837 897 49 477 657 342 717 454 511 559 169 259 394 213 d ઠે q ò g 8 d ò g ò g ò 셤  $\dot{\delta}$ g ò g à ò d ò 776 453 ---AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603 GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510 GARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558 897 GPAGKSGDRGETGPAGPÁGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLÓ 956 GAAGRVGPPGPPGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP DB 15; Length 1171; Version #1.30 Query Match
Best Local Similarity 60.2%; Pred. No. 2.1e-104;
Matches 441; Conservative 23; Mismatches 152; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

SOFTWARE: Patentin Release #1.0, Ver

SOFTWARE: Patentin Release #1.0, Ver

RELICATION DATA:

APPLICATION NUMBER: US/10/104,889

FILING DATE: 22-Mar-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

RILING DATE: 09-0CT-1998

ATTORNEY/AGNET INFORMATION:

NAME: STEEN, JEFFREY S

TELECOMMUNICATION: TOPOLOGY: unknown ULE TYPE: peptide NCE DESCRIPTION: SEQ ID NO: 8: TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
AMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS: LENGTH: 1171 amino acids STRANDEDNESS: single ZIP: 11553 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy GPPGPPGPPGPPG 1029 GDLGAPGPSGPAG 616 U.S.A. GPPGP----STATE: NY COUNTRY: U , MOLECULE ; SEQUENCE 1 US-10-104-889-8 INFORMATION RESULT 3 US-10-104-889-8 717 454 1017 777 837 511 559 604 394 Dp 8 g à g ò g δ ò 임

393

----AGVMGFFGPKGAAGEPGKAGERGVPGPPGA----

776

300 959 341

258 596

536

168

356

-GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA

212

453 836 510 926

-----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603

558

-----AGAQ

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| ΩÞ                   | 957 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1016   | w |
| λŏ                   | 604 GDLGAPGPSGPAG 616   |   |
| qq                   | 1017 GPPGPPGPPG 1029  |   |
| RESULT 4             | 4   |   |
| US-10-10             | US-10-104-889-10  |   |
| , Sequer<br>, Public | Sequence 10, Application US/10104003<br>Publication No. US20040086961A1 |   |
| GENE                 | GENERAL INFORMATION:  |   |
|                      | APPLICANT: GRUSKIN, ELLIOT A.   |   |
|                      | BUECHTER, DOUGLAS   |   |
| <b>.</b>             | BROKAW, JANE  |   |
|                      | ZHANG, GUANGHUI   |   |
|                      | PAOLEILA, DAVID   |   |
|                      | TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES                    |   |
| . •-                 | NUMBER OF SEQUENCES: 50   |   |
|                      | CORRESPONDENCE ADDRESS:   |   |
|                      | ADDRESSEE: DILWORTH & BARRESE   |   |
|                      | STREET: 333 EARLE OVINGTON BOULEVARD                                    |   |
| . •-                 | CITY: UNIONDALE   |   |
|                      | STATE: NY   |   |
| . •-                 | COUNTRY: U.S.A.   |   |
|                      | ZIP: 11553  |   |
|                      | COMPUTER READABLE FORM:   |   |

Gaps

117;

Indels

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Sequence 21, Application US/10216705

| Sequence 21, Application US/2030096973A1
| General Information No. US20030096973A1
| General Information:
| APPLICAMY: Maristem Therapeutics, S.A. |
| TILLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Me |
| TILLE OF INVENTION: Obcaining Such and Their Uses |
| TILLE OF INVENTION: Description of the company of the company
                                                                               698 GANGAPGNDGAKGDAGAPGAPGAPGAPGLQGNPGERGAAGLPGPKGDRGDAGPKGADGSP 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGSPGKTGPPGPAGQDGRPGPPGPPGAKGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGERGEOGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   638 GSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPP-----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                          1017 GPPGPPGPPGPPG 1029
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US-10-216-705-21
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Best Local S:
Matches 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PGP---- 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 64.1%; Score 2237.5; DB 15; Length 1388; Best Local Similarity 60.2%; Pred. No. 2.3e-104; Matches 441; Conservative 23; Mismatches 152; Indels 117; Gaps
                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION AUTHORN.
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-CCT-1998
ATPORTATION NUMBER: US/09/169,768
FILING DATE: 09-CCT-1998
ATPORMEY/AGENT INFORMATION:
NAME: STEEN, UFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8816
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1888 main a cids
TYPE: anin a cids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Page 5

| Db 938 GADGPAGAPGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 997  Qy 454 GPAGPKGSPGEAGRPGEAGLPGAKGILTGSPGSPGPDGKTGPPGPAGDGRPGPPP 510 | Oy 604 GDLGAPGPSGRAG 616  Db 1178 GPPGPPGPPG 1190  RESULT 7  US-10-358-024-1 ; Sequence 1, Application US/10358024 ; Publication No. US20040151732A1 ; Sequence 1, Application US/10358024 ; Publication No. US20040151732A1 ; APPLICANT: Delsue, Stephen ; TITLE OF INVENTION: Methods and Compositions Involving Blood ; TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen ; FILE REPERENCE: 13436US ; CURRENT APPLICATION NUMBER: US/10/358,024 ; CURRENT APPLICATION NUMBER: US/10/358,024 ; NUMBER OF SEQ ID NOSE: 3 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 1 ; LENGTH: 1464 ; TYPE: PRT ; ORGANISM: Home Sapien   | Query Match         64.1%;         Score 2237.5;         DB 16;         Length 1464;           Best Local Similarity         60.2%;         Pred. No. 2.4e-104;         Pred. No. 2.4e-104;         Pred. No. 2.4e-104;           Matches 441;         Conservative         23;         Mismatches         152;         Indels 117;         Gaps         12;           Qy         1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48  | Oy 49 GPKGSPGEAGRPGEAGLFGAKGLTGSPGSPGPDGKTGPPGAGQDGRPGPPGARGQA 108  | Qy         169 GSPGFQGLPGPAGEPGEAGKPGEQGVPGDLGAPGPSGPAGEPGP         212           Db         638 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPR 697           Qy         213TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPPAGPRGSP           Db         698 GANGAPGNDGAKGDAGAPGSQAPGLGAPGLGAPGLGAPGLGAPGBRGSPPAGPKGDAGPKGAGPKG | Qy 259 GEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP 300 | Oy 301 GPPGPPGARGOAGVMGPPGPKGAAGEPGKAGERGVPGPPGA 341  Db 818 GADGQPGAKGEPGDAGAKGDAGPPGPAGPPGPTGNVGAPGAKGARGSAGPPGATGFP 877  Qy 342VGPAGKDGEAGAGPPGPAGPAGERGEQGPAGSPGFPGFP 393  |
|---|---|--|---|---|---|--|
| Db   998   GPMGPPGLAGPPGESGREGAPGAEGSPGRDGSPGAKGDRGETGPAGPPCAPGAPGAPGAP   | RESULT 6  US-10-357-851-1  Sequence 1, Application US/10357851  Publication Wo. US20040151731A1  Publication Wo. US20040151731A1  APPLICANT: Jicha, Douglas L.  APPLICANT: Jicha, Douglas L.  TITLE OF INVENTION: Method and Compositions Involving  TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue of  TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients  TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients  TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients  CURRENT PILING DATE: 2003-02-04  NUMBER: OF SEQ ID NOS: 3  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 1  LENGTH: 1464  TYPE: PR  ORGANISM: Homo Sapiens  US-10-357-851-1  Query Match  G4.1%; Score 2237.5; DB 16; Length 1464;  Matches 441: Conservative 6.2%; Pred No. 2.49-104;  Matches 441: Conservative 6.2%; Pred No. 2.49-104; | Company   Comp | QY         109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGBAGKDGBAGAQGPPGFAGFAGERGEQGPA 168           Db         578 GVMGFPGPKGAAGEPGKAGERGVPDCPPGAVGPAGKDGEAGAAGEPGPAGERGEQGPA 637           QY         169 GSPGFQGLPGPPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPPGP | QY         213  |   | Qy         342        VGPAGKDGEAGAQGPPGPAGPAGERGEOGPAGSPGFQGLPGPAGPPGEAGKP         393           Db         878         GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGFPGEVGPPGPPGPAGKGSP         937           Qy         394         GEQGVPGDLGAPGPSGPAGFPGPTGLPGPPGREGGPGSRGFPGADGVAGPKGPAGERGSP         453           Qy         1 |

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1058 dPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1117
                                                                                                                                                                                                                                                                                                                                                                                                                            GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP 510
                                                                                                                                                                                                                                                                                                                           511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ 558
        GVMGFPGPKGAAGEPGKAGERGVPGPPGA---- 341
                                                                                  ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                              GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
                                                                                                                                                                                                                                                                                                                                                                                                         ----AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                        818 GADGQPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFP
                                                                                                                      878 GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 GARGEPGPAGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Seeley, Todd W.
TITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS
FILE REFRENCE: FP0402.3 CON
CURRENT APPLICATION NUMBER: US/10/402,089
CURRENT APPLICATION NUMBER: US 09/709,700
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR RILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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62.0%; Pred. No. 3.6e-104;
ive 21; Mismatches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/10402089; Publication No. US20040005663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1178 GPPGPPGPPG 1190
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Matches 438; Conservative
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CRGANISM: Sus scrofa
US-10-402-089-8
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US-10-402-089-8
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 150, Application US/10788792
Publication No. US20040191819A1
GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Busine Discount of the Corporation
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
FILE REFERENCE: 515
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT APPLICATION NUMBER: US 60/450,655
PRIOR APPLICATION NUMBER: US 60/450,655
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.2
SEQ ID NO 150
                                                                                                                                           1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPV 1177
                                                                                                                                                                                                                                      1058 GPAGKSGDRGETGPAGPAGPVGPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLØ 1117
                                                                                                                    GPAGP----KGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPP 510
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GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP 937
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                                                                 511 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE------AGAQ
                                                                                                                                                                                                                                                                                GPPGP------AGPAGERGEQGPAGSP---GFQGLPGPAGEPGEAGKPGEQGVP
                                        GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                  1178 GPPGPPGPPG 1190
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CRGANISM: Homo sapiens
US-10-788-792-150
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                                        394
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711
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652 GPPGEAGKPGEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAK
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Best Local Similarity 60.0%; Pred. No. 3.8e-104;
Matches 440; Conservative 23; Mismatches 153; Indels 117; Gaps
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                                     213 --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-
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| Publication No. U920040157329A1
| GENERAL INFORMATION:
| APPLICANT: ADP Pharmaceutical Pty Limited
| APPLICANT: The University of Sydney
| TITLE OF INVENTION: Matrix gene expression in cho;
| FILE REFERENCE: 500311
| CURRENT APPLICATION NUMBER: US/10/468,091-
| CURRENT FILING DATE: 2003-08-13
| PRIOR APPLICATION NUMBER: AU PR3116
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: Patentin version 3.1
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-468-091-25
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 GRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGP---PGPPGARGQAGVMGF-
                                                                                                                                   ---PGPXGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPPGPAGE
                                                                                                                                                                                                           ---RGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGP
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Polarek, James W.
APPLICANT: Polarek, James W.
TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS FILE REFERENCE: FP0402.2 CON
CURRENT APPLICATION UNMBER: US/10/402,072A; CURRENT FILING DATE: 2003-03-05
FRIOR APPLICATION NUMBER: US 09/709,700
FRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH. 4140
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Pred. No. 3.6e-104;
1; Mismatches 154;
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ilarity 62.0%;
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US-10-402-072A-8
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Best Local Simi:
Matches 438;
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TYPE: PRT
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  158 GPPGPAGEEGKKGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 517
                                                                                                                                                                                                                                                                                -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP 258
                                                                                                                                                                                                                                                                                                                                                            GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
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                                                                                                                                                                                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                               518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
                                                                                                                     GVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAOGPPGPAGPAGERGEOGPA
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BROKAM, JANBE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
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COMPUTER: IBM PC compatible
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US-10-1.4.
10S-10-1.6.
1 Sequence 16, Application US/10104889
1 Publication No. US20040086961A1
1 GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
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APPLICANT: Hyseq. Inc.
APPLICANT: Tang et al
TITLE OF INVENTION: NO. US20030232054Alel Nucleic Acids and Polypeptides
TITLE OF INVENTION: NO. US20030232054Alel Nucleic Acids and Polypeptides
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/41,404
PRIOR PLILING DATE: 2000-01-25
PRIOR PLILING DATE: 2000-01-25
PRIOR PLILING DATE: 2000-01-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PLILING DATE: 2000-09-015
PRIOR FILING DATE: 2000-09-015
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
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935 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 994
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                                                          -TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
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Publication No. US20030232054A1
GENERAL INFORMATION:
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US-10-291-265-243
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US-10-291-265-243
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INFORMATION FOR SEQ ID NO: 18 SEQUENCE CHARACTERISTICS
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US-10-058-124-18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-104-889-16
                                                                                                                                                                               NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                 TELEFAX: (516) 228-8516 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 60.0%
Matches 440; Conservative
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Carrying Out to the Presence of
GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGFV 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA 108
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                                                                                                                                                                                                                                      Sequence 18, Application US/10058124
Publication No. US20030119058A1
GENERAL INPORMATION:
APPLICANT: Qvist, Per
Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
Method and Use of the Method to Disgnose Method and Use of the Method to Disgnose Disorders Associated with the Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14;
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63.9%; Score 2228.5; DB 14
Best Local Similarity 60.0%; Pred. No. 6.4e-104;
Matches 440; Conservative 23; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W5-DOS
SOFTWARE: PATENTIN Release #1.0, Ve-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CLASSIFICATION: <unh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 08/187,319
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: COLLAGEN ALPHA 1 (I)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ^{R}
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P
STREET: 805 Third Avenue
CITY: New York
STATE: New York
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                                                     GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                          -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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                                                                                                                                                                                                                                                                                                                                  574 GANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
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Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad & C. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Renneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: 60/22,599

PRIOR PLICATION NUMBER: 60/22,599

PRIOR PLICATION NUMBER: 60/224,360

PRIOR PLICATION NUMBER: 60/224,360
                                                                                                                                   GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
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US-09-918-715-261
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US-09-918-715-261
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Length 1464;

DB 10;

Score 2227.5;

63.98;

Query Match

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1118 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            998 GPMGPPGLAGPPGESGREGAPAAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPV 1057
                                                                                                                         517
                                                                                                                                                                              108
                                                                                                                                                                                                                   518 GPKGSPGBAGRPGBAGLPGAKGLTGSPGSPGSPGKTGPPGPAGQDGRPGPPGPPGARGQA 577
                                                                                                                                                                                                                                                                             GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGBAGERGEQGPA 168
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                                                                                                                                                                           GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 GANGAPGNDGAKGDAĞAPGAPGAÇGAPGLQGMPGERGAAGLPGPKGDRGDAĞPKGADGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             878 GAAGRVGPPGPSGNAGPPGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
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                                                                         GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              818 GADGOPGAKGEPGDAGAKGDAGPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                             Gaps
                             117;
                       Indels
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Pred. No. 7.7e-104; ; Mismatches 154;
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Job time : 84.3776 secs
Best Local Similarity 59.9%; Pr.
Matches 439; Conservative 23;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 18, 2004, 13:31:10 ; Search time 24.4569 Seconds (without alignments) 2427.363 Million cell updates/sec

US-10-658-989A-2 3488 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 617 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|               | alpha 1(I | H        | <u>,</u> | ï        | 7        | 7    | 1(     | 7        | 1       | 7 (     | pha 1′(  | pha 1(I | pha 1(I | pha 1(I        | н<br>К  | æ       | æ       | æ       |         |         | pha 1 (V |         |               |         | Н       | N       | pha 5(I  |         | pha 1 (V |
|---------------|-----------|----------|----------|----------|----------|------|--------|----------|---------|---------|----------|---------|---------|----------------|---------|---------|---------|---------|---------|---------|----------|---------|---------------|---------|---------|---------|----------|---------|----------|
| tion          | ٠.        |          |          |          |          |      |        | n<br>J   | n al    | r<br>B  | E<br>G   | า<br>ผู | กลไ     | กลา            | n<br>a  | n<br>al | ager    | n<br>a] | n<br>a] | n<br>al | n<br>a]  | n<br>aJ | n<br>aJ       | n<br>a] | n<br>a] | ᇤ       | ื่อ<br>ไ | [<br>답  | n<br>a]  |
| Descript      | lag       | collagen | collagen | collagen | collagen | ä    | ิซ     | collagen | collage | collage | collage  | collage | collage | collagen alpha | collage | collage | procell | collage |         |         | collage  |         |               | collage | collage | collage | collage  | 덩       | collage  |
|               |           |          |          |          |          |      |        |          |         |         |          |         |         |                |         |         |         |         |         |         |          |         |               |         |         |         |          |         |          |
|               |           |          |          |          | -        |      |        |          |         |         |          |         |         |                |         |         |         |         |         |         |          |         |               |         |         |         |          |         |          |
| Ωï            | CGHU1S    | 521626   | CGCH18   | CGRT1S   | T45467   | ₽    | A41182 | m        | 검       | B40333  | A40333   | 859856  | CGB07S  | CGHU7L         | I50694  | CGHU2V  | I49607  | A43291  | CGHU2S  | CGHUIV  | S18803   | CGHUIE  | 823809        | 828774  | \$18251 | CGHU2E  | 822917   | ೧೯೮೦ ೧೮ | A54849   |
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| Length        | 46        | LΩ.      | 94       | ~        | 1418     | 48   | 41     | 48       | 7       | 8       | $\omega$ | ro.     | 04      | ø              | œ       | a)      | σ       | 37      | 36      | 83      | ゼ        | 80      | 41            | 02      | 0       | 54      | o        | 673     | 4        |
| 당선            | 63.9      | 63.2     | ä        | ~        | 55.7     | 55.7 | 55.4   | 55.4     | 4.      | 4.      | 4.       | щ       | ო       | m.             | ά,      | ď,      | ή.      | ä       | ö       | φ,      | 48.4     | 7.      | •             | •       | 'n      | ٠       | 45.4     | ď.      | 45.0     |
| ŭ             | 228.      | 205.     | ä        | 011,     | SH       | 94   | 93     | m        | 9       | °.      | മ        | 7.      | 85      | 85             | 4       | ď       | 80      | 8       | 16      | 02.     |          | 64      | o.            | 61      | 58      | 58      | 58       | 1583.5  | 56       |
| Result<br>No. | 1         | 0        | m        | 4        | ī.       | 9    | 7      | 80       | 6       | 10      | 11       | 12      | 13      | 14             | 15      | 16      | 17      | 18      | 19      | 20      | 21       | 22      | 23            | 24      | 25      | 26      | 27       | 28      | 29       |

| type VII collagen | collagen alpha 1(X | collagen alpha 4(I | collagen alpha 2(I | collagen alpha 2(I | collagen alpha 1(I | collagen alpha 1(V | collagen alpha 1(X | collagen alpha 1(I | collagen alpha 3(I | collagen alpha 2(I | collagen COLF1 - f | collagen alpha 2(I | hypothetical prote | collagen alpha 1(X | collagen alpha 3(I |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 148103            | S28791             | CGHU1B             | 516366             | CGCH2S             | CGHU4B             | A45748             | S23810             | CGMS4B             | CGHU3B             | CGHU2B             | S31521             | T29351             | T29350             | JX0369             | A45407             |
| N                 | 0                  | Н                  | ~                  | Н                  | -                  | ~                  | 7                  | Н                  | н                  | ч                  | N                  | N                  | N                  | N                  | N                  |
| 1549              | 888                | 1690               | 1763               | 964                | 1669               | 920                | 1603               | 1669               | 1670               | 1712               | 812                | 1759               | 1758               | 1142               | 1752               |
| 44.6              | 44.5               | 44.4               | 43.9               | 43.8               | 43.6               | 43.3               | 43.2               | 43.1               | 42.7               | 42.5               | 42.2               | 41.9               | 41.8               | 41.7               | 41.2               |
| 1556.5            | 1550.5             | 1547               | 1530               | 1526               | 1522               | 1510               | 1508               | 1503.5             | 1489.5             | 1481               | 1471.5             | 1463               | 1459.5             | 1456               | 1437.5             |
| 30                | 31                 | 32                 | 33                 | 34                 | 3                  | 36                 | 37                 | 38                 | 6<br>6             | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

# ALIGNMENTS

RESULT 1 CGHUIS

|   | collagen alpha [1] chain precursor - numan  |
|---|---|
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|   | N/Aireiliace liames: procoliagen alpia i/i/ chain   |
|   | Cispecies: Homo sapiens (man)   |
|   | C,Date: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004   |
|   | , , , , ,   |
|   | 5269; A29439; I53466; A02852; I37247  |
|   | a 'anorı  |
|   | Gene 67, 105-115, 1988  |
|   | A, Title: Complete nucleotide sequence of the region encompassing the lirst twenty-live   |
|   | A, Reference number: 160114; MUID:88329734; PMID:2843432  |
|   | A,Accession: I60114   |
|   | A;Status: translated from GB/EMBL/DDBJ  |
|   | A; Molecule type: DNA   |
|   | A;Residues: 1-369,'L',371-589 <dal></dal>   |
|   | A, Cross-references: UNIPROT: P02452; UNIPROT: Q14992; UNIPROT: Q16053; UNIPROT: Q13896; UNI  |
|   | R,Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Proc.  |
|   | Biochem J. 253, 919-922, 1988   |
| _ | A; Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human  |
|   | A: Reference number: S01143; MUID: 89025644; PMID: 3178743  |
|   | A.Accession: S01143   |
|   | A:Molecule type: mRNA   |
|   |   |
|   | 1. Cross_reference: EMRI.x07884: NID: 030015: PIDN: CAA30731.1; PID: 030016; GB: M36546; NI   |
|   | A. Morto. Carle to the EMBL/GenBank/DDRI databases by Prockob. D.J., 13-JUN-1988  |
|   | Affore: Bubilitheed to the binary district accounting to the first of |
|   |   |
|   | Nature 310, 33/-340, 1904   |
|   | COLLAGOR Selle Structure reveals evolutionals conscious   |
|   | , 655584  |
| _ | A;Accession: A93335   |
|   | A; Molecule type: DNA   |
|   | A;Residues: 1-58,'Q',60-181 <chu></chu>   |
|   | 4   |
|   | R;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Kamlrez, F.; de Wer, W   |
|   |   |
|   | דדמקפוו קפוום   |
|   | A, Reference number: 155254; MUID:88033098; PMID:2822/14  |
|   |   |
|   | A,Status: translation not shown; translated from GB/EMBL/UDBU   |
|   | A, Molecule type: DNA   |
|   | 0000  |
|   | 217.91803   |
|   | R;Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, K.E.  |
|   | Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987   |
|   | elements in the first intron contribute to transcributional   |
|   | A; Reference number: A39943; MUID:88097389; PMID:3480516  |
|   | A;Accession: A39943   |
|   | A, Molecule type: DNA   |
|   | CCC332.010  |
| _ | A; Cross-references: GB:J03559; NID:91808/6; FIDN:AAA52052.1; FID:9553536   |
| _ | R;Chu, M.L.; de Wet, W.; Bernard, M.; Kamirez, F.   |

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Biol. Chem. 260, 611-694, 1985
Title: Multiexon deletion in an osteogenesis imperfecta variant with increased type II: Reference number: A22161; MUID:85104934; PMID:2981843
                                                                                      A; Molecule type: mRNA
A; Residues: 342-352, CC', 354-359 - MIZ>
A; Cross-references: GB: S64717; NID: 9406195; PIDN: AAB27677.1; PID: 9408196
A; Note: mutant sequence from patient with osteogenesis imperfects
R; Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-523, 1988
A; Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A; Reference number: A90476; MUID: 84080385; PMID: 6689127
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A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:9407589; PIDN:AA227856.1; PID:9407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different mut
A;Accession: B47426
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A,Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Cobn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Ni J. Biol. Chem. 263, 14605-14607, 1988
A.H.Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide A; Reference number: 155269; WUID:89008319; PMID:3170557
A.Accession: 155269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN: AAA51847.1;
                                                                                                                                                                                                                                                                                                                                                              Accession: A90476
Molecule type: mRNA
Molecule
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A; Residues: 1179-1387, 'R', 1389-1464 <CH7>
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A;Residues: 1179-1276,'H',1278-1464 <CH5>
A;Experimental source: fetal cell 86-237
A;Accession: D47426
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                                                             tatus: translated from GB/EMBL/DDBJ
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A,Residues: 1179-1336,1339-1464 <CH6>
A,Experimental source: fetal cell 86-:
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Residues: 1179-1464 <CH4>
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A;Title: Multiexon de
A;Reference number: 7
A;Accession: A22161
                                A; Accession: I52905
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A, Molecule type: mRI
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A; Residues: 259-268,1347-1357 cDEA>
A; Residues: 259-268,1347-1357 cDEA>
A; Residues: 259-268,1347-1357 cDEA>
A; Residues: 259-268,1347-1357 cDEA>
A; Cross-references: GB:S67-495; NID:9239007; PIDN:AAB20350.1; PID:9239008
A; Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
A; Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
B; More: accomparative study of glycopeptides derived from selected vertebrate collagens.
A; Reference number: A92069; MUID:71001508; PMID:4319110
A; Reference number: A92069; MUID:71001508; PMID:4319110
A; Residues: 26-268 cMOR>
A; Residues: 26-268 cMOR>
A; Residues: 26-268 cMOR>
A; Residues: 26-268 cMOR>
A; Residues: 25-268 cMOR>
A; Residues: 25-268 cMOR>
A; Residues: 25-268 cMOR>
A; Reference number: S15989; MUID:90326017; PMID:2374517
A; Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A; Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A; Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 cLAB>
A; Reference number: Issue Res. 29, 1-11, 1993
A; Rittle: A cysteine for glycine substitution at position 175 in an alpha 1 (1) chain of A; Reference number: IS2905; MUID:93339642; PMID:8335941
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Biol. 14, 593-595, 1994
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Best Local Similarity
Matches 432; Conserv
                                                                                                                domain.
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collagen alpha 1(I) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S57243; S16374; A23992; I49559; I49557; S39789; I48300; S21626
R;Li, S.W.; Khillan, J.; Prockop, D.J.
                                                                                                                                                                                                                                578 GVMGFPGPKGAAGERGKAGERGVPGPPGANGPAGKDGEAGAGGPFGPAGPAGERGEQGPA
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                A, Molecule type: DNA
A, Residues: 1187-1194, C', 1196-1220 COH>
A, Residues: 1187-1194, C', 1196-1220 COH>
A, Cross-references: GB: M23213; NID: 9346842; PIDN: AABS9363.1; PID: 9499622
A, Note: mutant sequence from a patient with mild osteogenesis imperfecta
R, Mackelae, J.K.; Raassina, M.; Virta, A.; Vuorio, B.
Nucleic Acids Res. 16, 349, 1988
A, Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptic
                                                                                                                                           Query Match 63.9%; Score 2228.5; DB 1; Length 1464; Best Local Similarity 60.0%; Pred. No. 4.2e-105; Matches 440; Conservative 23; Mismatches 153; Indels 117;
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A, Generics:
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A, Generics:
Collagen alpha 1(1) Chain, fibrillar collagen carboxyl-terminal homology
C, Superfamily: collagen alpha 1(1) Chain, fibrillar collagen carboxyl-terminal homology
C, Superfamily:
C, Gewonds:
C, Gewonds:
C, Generics:
C, Gewonds:
C, Gewonds:
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A,Residues: 1-80,'E',82-105,'D',107-147 <REF>
A,Cross-references: EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID:950487
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llarity 58.9%; Pred. No. 6e-104;
Conservative 22; Mismatches 162; 1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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collagen alpha 1(I) chain - rat (tentative sequence) (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
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COLIAGEN 1(I) chain - chicken (tentative sequence) (fragments)
Cyspecies: Gallus gallus,(chicken)
C;Species: Gallus gallus,(chicken)
C;Species: Gallus gallus,(chicken)
C;Species: Gallus gallus,(chicken)
C;Date: 12-Aug-1981 #sequence_revision 06-Jul-1982 #text_change 31-Mar-2000
C;Accession: A00458; A90181; A202857
R;Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J. Biochemistry 21, 2048-2055, 1982
A;Title: Amino acid sequence of chick skin collagen alphal(I)-CB8 and the complete prima A;Accession: A90458
A;Molecule type: procein
A;Residues: 1-1036 <-HIG-
A;Residues: 1-1036 <-HIG-
A;Residues: 1-1036 <-HIG-
A;Residues: acidest in a series of papers from these workers elucidating the sequence this is the latest in a series of papers from these workers elucidating the sequence Biophys. Res. Commun. 48, 720-726, 1972
A;Title: Evidence for a previously undetected sequence at the carboxyterminus of the alp A;Reference number: A90181; MUID:72243016; PMID:5047697
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|||| GPPGPAGEEGKRGARGEPGPSGLPGPPGERGGPGSRGFPGADGVAGPKGPSGERGAPGPA
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-GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                     GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGERGEQGPA
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A; Molecule type: protein
A; Residues: 1037-1042 < EDRs
A; Residues: 1037-1042 < EDRs
A; Residues: 1037-1042 above correspond to the carboxyl end of the protein
A; Note: residues 1037-1042 above correspond to the carboxyl end of the protein some C; Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in some C; Comment: Most of the profilines at the third position of the tripeptide repeating unit (C; Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in poc; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 GADGQPGAKGETGDAGAKGDAGPPGPAGPTGAPGPAGZVGAPGPKGARGSAGPPGATGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPGAVGPAGKDGEAGAQGPPGPAGPAGE - - - RGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAGP --- KGSPGBAGRPGBAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPAGPPGARGQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 GANGAPGNDGAKGDAGAPGNEGPPGLEGMPGERGAAGLPGAKGDRGDPGPKGADGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGRVGPPGPSGNIGLPGPPGPAGKZGSKGPRGETGPAGRPGEPGPAGPPGEKGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 2151.5; DB 1; Length ed. No. 2.4e-101; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score Pred. ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 57.8%; Pre 424; Conservative 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.7%;
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Best Local Similarity
Matches 424; Conserv
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Tue

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A; Restduces: 568-51 <511.>
A; Restduces: 568-51 <511.>
A; Restduces: 568-51 <511.>
A; Restduces: 568-51 <511.>
A; Note: this region probably corresponds to positions 949-1032 of the alpha 1(I) chain A; Note: the major antigenic determinant (of neutral salt-extracted rat skin collagen) i R; Stoltz, M.; Timpl, R.; Kuehn, K.
FEBS Lett. 26, 61-65, 1972
A; Title: Non-helical regions in rat collagen alphal-chain.
A; Reference number: A91385; MUID:73049495; PMID:4656751
A; Reference number: A91385
A; Molecule type: protein
A; Residuces: 651-671 <672>
A; Experimental source: skin
A; Residuces: 651-671 above) probably corresponds to positions 1032-105
C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit and subsequently 0-glycosylated.
C; Comment: The order of the nine CMBr peptides in the alpha 1(I) chain of rat skin coll c; Comment: The order of the nine CMBr peptides in the alpha 1(I) chain of rat skin coll C; Comment: The complete chain contains 1052 residues.
C; Superfamally: collagen alpha 1(I) dain; fibrillar collagen carboxyl-terminal homology C; Keywords: blocked amino end; Coll; extracellular matrix; glycoprotein; hydroxyl C; Reywords: blocked amino end; colled coll; extracellular matrix; glycoprotein; hydroxyl F; 103,424,547/Binding site: carbohydrate (Lys) (covalent)
F; 103,424,547/Binding site: 5-hydroxylysine (Lys) (partial) #status experimental
F; 424,547/Modified site: 5-hydroxylysine (Lys) (partial)
A; Residues: 419-567 < BU3>
A; Residues: 419-567 < BU3>
A; Reparimental source: skin
B; R; A; Eparimental source: skin
B; R; Coltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 37, 287-294, 1973
A; Titles: Structural and immunogenic properties of a major antigenic determinant in neut
A; Reference number: A91209; MUID:74011954; PMID:4126850
A; Accession: A91209
A; MulD:74011954; PMID:4126850
A; Mesadues: 568-651 < CTIP
A; Residues: 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 GEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQGPSGAPGPK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPGDLGAP------GPSGPA-----GEPGPTGLPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 GNSGEPGAPGNKGDTGAKGEPGPAGVOGPPGPAGEEGKRGARGEPGPSGLPGPPGERGGP
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59.5%; Pred. No. 1.8e-94;
iive 28; Mismatches 119; Indels 123;
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Best Local Similarity 59.5'
Matches 396; Conservative
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Biochemistry 8, 63-71, 1969
A,Title: Comparative Sequence studies of rat skin and tendon collagen. II. The absence c A,Reference number: A90559, MUID:69155173; PMID:5777344
A,Contents: CNBYO and CNBY1
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;Residues: 239-418 eRbs.
;Reserimental source: skin
;Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
iochemistry 13, 2946-2953, 1974
;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
;Reference number: A90379; MUID:74271984; PMID:4366532
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A; Readudes: 10-15 = ROS
A; Rexperimental source: skin and tendon
A; Experimental source: skin and tendon
B; Butler, W.T.; Ponds, S.L.
Biochemistry 10, 2076-2081, 1971
A; Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino
A; Reference number: A90353; MUID:71263178; PMID:4327399
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Afresidues: 1-19 < 4801>
Afresidues: 1-10 < 480
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A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The
A;Reference number: A90566; MUID:70085124; PMID:5411206
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A, Title: The incomplete hydroxylation of individual prolyl residues in collagen.
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A, Contentes: CNBr2
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A,Molecule type: protein
A,Residues: 56-102 <BU1>
A,Experimental source: skin
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A;Contents: CNBr3
A;Accession: A90379
A;Molecule type: protein
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R,Bornstein, P.
J. Biol. Chem. 2
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A;Note: mutant sequence associated with perinatal lethal hypochondrogenesis
F;Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
Proc. Natl. Acad. Sci. US.A. 87, 38893, 1990
A;Title: Tandem duplication within a type II collagen gene (COLZAI) exon in an individu A;Reference number: S16502; MUID:90251662; PMID:2339128
A;Accession: S16502
A;Molecule type: DNA
A;Residues: 1164-1184, GPSGKDGANGIPGPI',1185-1199 <TIL2>
A;Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
A;Coss.references: EMBL.;M37126, NID:9180808; PIDN:AA$2037.1; PID:9180809
A;Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R;Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grossvld, F.G.; Solomon, E.
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A;Title: Identification and characterization of the human type II collagen gene (COLZAI)
A;Reference number: A02858; MUID:85190534; PMID:3857598
A;Accession: A02858; MUID:8190534; PMID:3857598
A;Accession: GB:J00116; NID:9180395; PIDN:AAA51997.1; PID:9180396
A;Cross-references: GB:J00116; NID:9180395; PIDN:AAA51997.1; PID:9180396
A;Title: Determination of the single polyadenylation site of the human pro-alpha-I(II)
A;Reference number: A27280; MUID:88067771; PMID:2825137
A;Title: Determination of the single polyadenylation site of the human pro-alpha-I(II)
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A; Molecule type: DNA
A; Mesidues: 1256-1338 AVUN2>
A; Mesidues: 1256-1338 AVUN2>
A; Cross references: 1288-MU2048; NID:9180017
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: the codons given for 133-Ly8 (AGG) and 1350-Gly (GCA) are inconsistent with th R; Sandioris, R: Sandioris, V. J. Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez Nucleic Acids Res. 13, 2207-2225, 1985
A; Title: Isolation and partial characterization of the entire human pro alpha 1(II) col A; Meseidues: 7-28, R., 99-114;541-578;786-802;1055-1056, N., 1058-1068, T., 1070-1109;1200-A; Molecule type: DNA
A; Residues: 7-28, R., 99-114;541-578;786-802;1055-1056, N., 1058-1068, T., 1070-1109;1200-A; Molecule type: DNA
A; Residues: 2-28 cANL2>
A; Molecule type: DNA
A; Residues: 7-28, MAL2>
A; Molecule type: DNA
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: J.244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A;Molecule type: C.M.; J.244-1246,'N', 1248,'X', 1250-1265;1295-1305;1395-1408 <VAN>
A;Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal pro
R;Strom, C.M.; Upholt, W.B.
Nucleic Acids Res. 12, 1025-1038, 1984
A;Title: Isolation and characterization of genomic clones corresponding to the human ty
A;Reference number: A21733; MUID:84118798; PMID:6320112
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A; Residues: 1245-1295 STR1>
A; Accession: B21733
A; Molecule type: DNA A; Molecule
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A.Recidues: 1175-1487 AEL1>
A.Recidues: A.R.
Biochem. J. 237, 923-925, 1986
A.Mitle: Chondrocalcin is identical with the C-propeptide of type II proc
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A;Status: translated from GB/EMBL/DDBJ
                          A,Title: Differential expression of a cysteine-rich domain in the amino-terminal propept A,Reference numbers na5428; MUID:90285153; PMID:2355003
A,Accession: A35428
A,Accession: A35428
A,Accession: A35428
A,Rolecule type: mRNA
A,Residues: 27-81, 10.3 < RYA2>
A,Note: alternative splice form 2; splicing appears to be under developmental regulation R,Xeu, MW.; Benson-Chanda, V: Vissing, H:; Ramirez, F.
Genomics 4, 438-441, 1989
A,Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide conf A,Accession: A3047
A,Reference number: A30147
A,Rolecule type: DNA
A,Residues: 104-157, VP, 159-236 <SUM>A,Residues: 104-157, VP, 159-236 <SUM
A,Residues: 111-172, CC, 174-175 <ALAA>
A,Rolecule type: DNA
A,Residues: 111-172, CC, 174-175 <ALAA>
A,Note: mutant sequence from a family with family with primary generalized osteoarthriti
B,Otaba, M, MU, JJ, Byra32, 1996
A,Title: Collagen type: IX from human cartilage: a structural profile of intermolecular CA, A, Accession: A, Reference number: Se44673; MUID:96195147; PMID:96302
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A;Reference number: 805000; MUD:89325561; PMID:2753125

A;Accession: 805000; MUD:89325561; PMID:2753125

A;Accession: 805000; MUD:89325561; PMID:2753125

A;Residues: 630-640, 'A', 642-785 «VIK2>

A;Residues: 630-640, 'A', 642-785 «VIK2>

A;Cross-references: EMB:136158; NID:923951; PIDN:CAA34278.1; PID:g1335018; PIDN:CAA3427

B;Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Byre, D.J.; Biol. Chem. 267, 22522-22526, 1992

A;Reference number: A44309; MUID:93054548; PMID:4429602
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A,Residues: 188-1499, X7, 1911-195,1224-1230, X7, 1232-1236 cDIA>
A,Residues: 188-1499, X7, 1911-195,1224-1230, X7, 1232-1236 cDIA>
B,Franc, S.; Marzin, B.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbage, Bur. J. Biochem. 234, 125-131, 1995
Bur. J. Biochem. 234, 125-131, 1995
A,Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil cax A,Reference number: 863514; MUID:96096730; PMID:8529631
A,Accession: 863514
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A/Status: preliminary, translated from GB/EMBL/DDBJ/
A/Status: preliminary, translated from GB/EMBL/DDBJ/
A/Residues: 440,'G',442-456,'E',458-480,'P',482-509 <TIL1>
A/Residues: 440,'G',442-456,'E',15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
R/Ramired From EMBL Data Library, December 1988
A/Reference number: S04892
A/Accession: S04892
A/Molecule type: mRNA
A/Residues: 501-676,'A',678-783,'A',785-831,'PA',834,'F',836-1214 <RAM>
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A/Residues: 501-676,'A',678-783,'A',785-831,'PA',836-1214 <RAM>
A/RESIDUE TYRED 
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A,Residues: 243-261;575-590,756-763,'X',765-779 <FRA>
R;Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, Hum. Genet. 56, 388-395, 10395
A;Title: An RNA-splicing mutation (G+SIVS20) in the type II colla A;Reference number: 138867; MUID:95150028; PMID:7847372
A;Accession: 138867
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procellagen

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A, Molecule type: DNA
A, Residues: 1-1419 (AET>
A, Cross-references: GB:MS-51, 1991
Bevelopment 111, 945-953, 1991
By Tritle: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilag A, Accession: A44885, MUD:91347939; PMID:1879363
A, Accession: A44885
A, Molecule type: DNA
A, Residues: 1-28 cdBs
A, Residues: 1-28 cdBs
A, Cross-references: GB:S63190; NID:g234368; PIDN:AAB19627.1; PID:g234369
A, Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
A, Cross-references: GB:S63190; NID:g234368; PIDN:AAB19627.1; PID:g234369
A, Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
C, Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C, Seywords: alternative splicing; collagen carboxyl-terminal homology FCC>
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  preliminary; not compared with conceptual translation
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                                                 GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
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collagen alpha 1(II) chain precursor - mouse
collagen alpha 1(II) chain precursor - mouse
collagen alpha 1(II) chain precursor - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
Cispecies: A. Marson, D. A. Marson, D. A. Marson, D. Ma
                                                                                                                                                                                                                                                                                                                                                                       344
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; Pred. No. 8.5e-91;
34; Mismatches 189; Indels 138;
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ilarity 52.1%;
Conservative 3.
                       Residues: 541-560 <SAN3>
Cross-references: EMBL:X02378;
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A; Molecule type: DNA
A; Residues: 541-560
A; Cross-references: E
A; Accession: 137251
  Molecule type: DNA
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Best Local Simil
Matches 393; C
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RESULT 9
Collagem alpha 1(1) chain - bovine (tentative sequence) (fragmente)
Collagem albha 1(1) chain - bovine (tentative sequence) (fragmente)
Collagem albha 1(1) chain - bovine (tentative sequence) (fragmente)
Collagem albha 1(1) chain - bovine (tentative sequence)
Collagem albha 1(1) chain - bovine (tentative sequence)
RANCESETOR - RESERVENCE - 1 (1902)
RANCESETOR - 1 (1904)
RANCESETOR - RAND - 1 (1904)
RANCESSOR - RAND - 1 (1904)
RANCES
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A,Residues: 759-779 «RA2»
A,Experimental source: 8kin
C,Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydro
C,Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are
                                             978
                         GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                          945
  583
     8 8
                                                              Collagen alpha 1(II) chain precursor (long splice form) - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: B4-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C.Accession: B41182
M. Piol. Chem. 266, 16862-16869, 1991
J. Biol. Chem. 266, 16862-16869, 1991
J. Biol. Chem. 266, 16862-16869, 1991
J. R.Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A;Reference number: A41182; MUD:91358489; PMID:1885613
A;Reference number: A41182; MUD:91358489; PMID:1885613
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: UNIPROT:062031; UNIPROT:062032; UNIPROT:062033; GB:M65161
C.Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C.Superfamin: von Willebrand factor type C repeat homology vWCo>
F;32-91/Domain: von Willebrand factor type C repeat homology vPCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.4%; Score 1932; DB 2; Length 1487;
Best Local Similarity 51.9%; Pred. No. 3e-90;
Matches 391; Conservative 36; Mismatches 189; Indels 138; Gaps
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A40333
collagen alpha 1'(II) chain precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accesion: A4033
F;Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
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B40333
C.John alpha 1(II) chain precursor - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Species: Xenopus laevis (African clawed frog)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: B4033
B.Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.
J. Cell Biol. 115, 565-575, 1991
A;Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis
     bovine
C,Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of boving 9, 149, 268, and 217 residues.
C,Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal ht C;Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                              54.4%; Score 1898; DB 1; Length 779;
53.0%; Pred. No. 9.6e-89;
ive 22; Mismatches 210; Indels 108;
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A, Reference number: A40333, MUD: 92011898; PMID: 1918153
A, Accession: B40333
A, Accession: B40333
A, Residuanty
A, Molecule type: mRNA
A, Molecule type: MRNA
A, Residuants: 1-1486 × SUA>
A, Residuants: 1-1486 × SUA>
A, Cross-references: WINPROT: 091718, UNIPROT: 091717, GB: M63595
A, Cross-references: WINPROT: 091718, UNIPROT: 091717, GB: M63595
A, Cross-references: UNIPROT: Collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology, Reywords: coiled coil; extracellular matrix; glycoprotesin; triner; triple helix
P, 137-96/Domain: von Willebrand factor type C repeat homology vVWC>
P, 1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 GLIGRPGDAGPQGKVGPSGASGEDGRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEK
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                                                                                                                                                                                                                                                                                                                                                                                      Length 1486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFQGLPGPAGPPGBAGKP-----GEQGVPGDLGAPGPS---GPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                  18.13 54.2%; Score 1890.5; DB 1; 18.15 54.6%; Pred. No. 3.6e-88; Conservative 40; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEAGKPGEQGVPGDLGAPGPSGPAG
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A,Reference number: A40333, MUID:92011898; PMID:1918153
A,Accession: A40333
A,Status: nucleic and as a squence not shown
A,Molecule type: mRNA
A,Fores: references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596
A,Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596
A,Note: this sequence is presented as substitutions relative to another sequence in a files they replace; the appropriate interpretation of the sequence figure was reconstructed C;Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homology; C;Reywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix F;37-96/Domain: von Willebrand factor type C repeat homology <WC>
F;1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FC>

13, 447 385 213 505 273 565 333 625 393 411 GDÓGVPGEAGAAGLVGPRGERGFPGERGSSGPQGLQGSRGLPGTPGTDGPKGATGPSGPN 745 51 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGAD-----GVAGPKGPAGERGSPGPAGPK GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM PGAVGPAGKDGEAGAQGPPGPAGPA GARGPEGAOGPRGESGTPGSPGPSGASGNPGTDGIPGAKGSSGASGIAGAPGFPGPRGPP GPQGATGPLGPKGETGDPG1AGFKGEHGPKGE1GSAGPQGAPGPAGEEGKRGARGEPGAA GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GLTGRPGDAGPQGKVGPSGAAGEDGRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEK GLGGAPGLRGLPGKDGETGAQGPNGPAGPRGERGEQGPPGPSGFQGLPGPPGSPGEGGKP -GAPGPSGPA ---GP-----GSRGFPGADGVAGPKGPA GPPGPQGARGFPGTPGLPGVKGHRGYPGLDGGKGEAGAAGAKGESGASGEAGAPGPMGPR GERGEQGP-----AGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPT GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP Gaps Score 1883; DB 2; Length 1492; Pred. No. 8.6e-88; 5; Mismatches 185; Indels 162; GFPGPKGAAGEPGKAGERGVPGP-46; GEPGPTGLPGPPGERG----54.0%; ilarity 49.1%; Conservative 46 GEOGVPGDL Similarity Best Local Simi Matches 379; 386 999 334 626 394 989 412 Query Match Best Local & 272 52 332 112 160 446 214 506 274 ò 임 ò d ò Op qq d Dp ò ద δ ò ò

865 513 573 985 805 471 GAPGPOGPSGAPGPOGPTGVNGPKGARGAQGPAGATGFPGAAGRVGTPGPNGNPGPPGPP 925 GAOGPPGLOGMPGERGAAGISGPKGDRGDTGEKGPEGAPGKDGSRGLTGPLGPPGPAGPN --- KGSPGEAGRPGEA GQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQ GSAGKEGPKGVRGDAGPTGRAGDPGLQGPAGAPGEKGEPGEDGPSGPDGPSGPQGLSGNR 919 ----GFQGLPGPAGPPGEAGKP---GEQGVPGDLGAPGPSGPAG GLPGAKGLTGSPGSPGPDGKTGP-GERGSPGPAGP-GPAGS P. 998 746 448 908 472 926 574 셤  $\dot{\delta}$ g à 유 δ 임 ò d ð  $\dot{\delta}$ 

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360

GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPA

301 755

GKDGP----RGPAGPIGPPGP---AGQPGDKGEGGSPGLPGIAGPRGGPGERGEHGPPGPA

754

408

GFPGAPGQNGEPGAKGERGAFGEKGEGGFPGPAGPTGSSGPAGPPGPQGVKGERGSPGPP

809

엄 ò

361

8

---GPAGERGEQGPAGSPGFQGLPGPAGPPGE---AGKPGEQGVPGDLGAPGPS

GTAGFPGGRGLPGPPGNNGNPGPPGPSGAPGKDGPPGPAGNSGSPGNPGIAGPKGDAGQP

GPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP

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646

GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK

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241 701

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GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP 

GEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA

586

chain precursor RESULT 12 S59856 collagen alpha 1(III)

C:Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text\_change 09-Jul-2004
C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text\_change 09-Jul-2004
C;Accession: S5956; SS2120; Si6373
R;Toman, P. D.; de Crombrugghe, B.
A;Aritle: The mouse type: III procollagen-encoding gene: genomic cloning and complete DNA
A;Resterance number: S59856; MUID:95011609; PMID:7926795
A;Accession: S59856
A;Accession: S59856
A;Accession: S59856
A;Accession: S5120
A;Accession: S6120
A;Accession: S6220
A; 9 467 GSPGEPCANGLPGAAGERGPSGFRGPAGPNGIPGEKGPPGERGFGPAGPRGVAGEPGRD GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP Gaps 93; Indels DB 2; 190; Score 1857.5; DB Fred. No. 1.6e-86; 39; Mismatches 190 53.3%; Conservative Similarity 369; Query Marc... 61 Best Loca Matches 음 ò

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A; Molecule type: protein

A; Molecule type: protein

A; Residues: 87-106;1017-1029;1037-1049 < HEN>

A; Residues: 87-106;1017-1029;1037-1049 < HEN>
C; Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h
C; Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C; Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C; Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C; Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C; Cyperfeminal pombelical properties caperimental cABB>
F; 1-1049/Product: collagen alpha I(III) chain; gitosprotein; hydroxylysine; hydroxylysine;
F; 15-1040/Region: cell attachment (R-G-D) motif
F; 15-1040/Region: cell attachment (R-G-D) motif
F; 17-1040/Region: cell attachment (R-G-D) motif
F; 17-1040/Region: cell attachment (R-G-D) motif
F; 104-1049/Region: cell attachment (R-G-D) motif
F; 104-1049/Region: cell attachment (R-G-D) motif
F; 104-1049/Region: cell attachment (R-G-D) motif
F; 107, 119, 938, 950/Modified site: 5-hydroxylysine (Lys) #status experimental
F; 107, 119, 938, 950/Modified site: 5-hydroxylysine (Lys) #status experimental
F; 107, 119, 1041/Disulfide bonds: interchain #status predicted
F; 1040, 1041/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GPAGPAGER 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 GAAGPPGPPGSAGTPGLQGMPGERGGPGGPGPKGDKGBPGSSGVDGAPGKDGPRGPTGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612 GPPGPAGOPGDKGESGAPGVPGIAGPRGGPGBRGEQGPPGPAGFPGAPGONGEPGAKGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 GEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGV-----PGDLGAPGPSGPAGEPGPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.2%; Score 1856; DB 1; Length 1049; 51.2%; Pred. No. 1.5e-86; ive 34; Mismatches 211; Indels 108;
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Best Local Similarity 51.2
Matches 371; Conservative
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                                                                                                                                                                                                                                                         GPPGAVGPAGKDGE------AGAQGPPGPAGERGEQGPAGSPGFQGLP
                                      ---AGLPGAKGLTGSPGSPGPDGKTGP
                                                                                                                                                                                                                                                                                                                                                                                                         GFPGNPGPPGSPGAAGHQGAIGSPGPAGPRG 1139
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A; Residues: 302-43 < CHT.
A; Residues: 302-43 < CHT.
B; Corst-references: GB: 879877; NID: 91195576; PIDN: AAB35615.1; PID: 91195577
B; Geyer; J.M.; Kang, A.H.
B; Covalent structure of collagen: amino acid sequence of five consecutive CNBr p
A; A; Reference number: A90114; MUID: 79000343; PMID: 687591
A; Reference number: A90114; MUID: 79000343; PMID: 687591
A; Residues: 309-675, W' 677-727 < CSEV3>
A; Reference number: A50144
A; Reference number: B549; MUID: 9116621; PMID: 1672129
A; Reference number: B5549; MUID: 9116621; PMID: 1672129
A; Reference number: A50414; MUID: 9116621; PMID: 1672129
A; Reference number: A50418; MUID: 9116621; PMID: 1672129
A; Reference number: A50418; MUID: 910980816
A; Reserver: J.M.; Mainardi, C.; Kang, A.H.
A; Reserver: J.M.; Mainardi, C.; Kang, A.H.
B; A; Reference number: A50438; MUID: 80198282; PMID: 6246925
A; Residues: 578-695; A' 897-964 < SEV4>
A; Residues: Broad: Broad:
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A; Residues: 965-979, A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157
A; Experimental source: liver
B; Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; My
Nucleic Acids Res. 12, 9383-9384, 1984
Nucleic Acids Res. 12, 9383-9384, 1984
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollag
A; Reference number: A93551; MUID:85087944; PMID:6096827
Am. J. Hum. Genet. 53, 62-70, 1993
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual fapring.
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual spring.
Ajritle: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual ajreaders.
Bj. Racession: IS1868
Ajritle: Parental spring MUID: 9304430; PMD: 8317500
Ajritle: Parental spring MID: 9386425; PIDN: AAD13937.1; PID: 94261637
Ajritle: Parental spring multiple Biochem J. 311, 939-943, 1995
Ajritle: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL Ajritle: Ajritle: SS9511; MUID: 96067614; PMID: 7487954
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with Ehlers-Danlos sy
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A,Status: translation not shown
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Rosiduse: 950-1018, Y',1020-1183, 'S',1185-1466 <MAN>
A,COSS-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
R,Seyer, J.M.; Kang, A.H.
B,Seyer, J.M.; Kang, A.H.
A,Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9
A,Reference number: A90446; MJID:81208139; PMID:7016180
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A, Residues: 861-1015 <COL>
A, Residues: 861-1015 <COL>
A, Cross-references: 861-1015 <COL>
A, Note: a mutant sequence with 942-977 spliced out from a patient
R, Mankco, B.S.; Dalgleish, R.
Mucleic Acids Res 16, 2337, 1988
A, Title: Human pro alphal(III) collagen: cDNA sequence for the 3'
A, Reference number: S02119; MUID:88189827; PMID:3357782
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A; Residues: 1-16 < BEN.
A; Residues: 1-176 < BEN.
A; Residues: 1-176 < BEN.
A; Cross-references: GB.N.26939; NID:g180813; PIDN:AAA52040.1; PID:g180814
A; Toman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre
A; Residues: S01726
A; MUD:88303360; PMID:3405773
A; Residues: S01726
A; MuD:88303360; PMID:3405773
A; Residues: L-170 < TOM>
A; Residues: L-170 < TOM>
A; Residues: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061
A; Note: the authors translated the codon CAG for residue 154 as His
A; Note: the authors translated and amino acid sequences of the entire human alpha-1 (III) collagen.
A; Reference number: S04887; MUD:89386015; PMID:2780304
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"Note: He authors' translation of residues 905-932 is inconsistent with the nucleotide from the surface of the second translation of residues 905-932 is inconsistent with the nucleotide incoherent in 118-1164, 1977

"Yorkler Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide treestion: A90399; MUID:77134724; PMID:557335
                                                                                                                                                                                                                                                                                                                                                   October alpha 1(III) chain precursor - human NyAlternate names: procollagen alpha 1(III) chain (Species to Ames: procollagen alpha 1(III) chain (Species to Ames: procollagen alpha 1(III) chain (Species to Amen sapiens (man) (Species to Amen sapiens (man) (Species to Amen sapiens (man) (Species to Amen subject to Amen subject to the EMBL Data Library, Pebruary 1989 (Species to Amen to Amen and Amen to Amen and Amen
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Residues: 'V,169-2232,29-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
A;Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galact
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A; Molecule type: mRNA
A; Residues: 1-1196 <ALA.
A; Cross-references: BML>X14420; NID: 930057; PIDN: CAA32583.1; PID: 930058
A; Acces: the complete sequence is not shown
R; Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
R; Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
A; Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene
A; Reference number: PE0011; MUID: 89378752; PMID: 2777083
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submitted to the Atlas, December 1977
A)Reference number: A94562
A)Accession: A94562
A)Accession: A94562
A)Accession: A94562
A)Recule type: protein
A)Recule type: protein
A)Repidues: 'V'.169-225,229-277,'A',279-292,'D',294,'S',296-398 <8EY2>
A)Reprimental source: liver
A)Roce: author submitted corrections to A90399
B)Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S04642; MUID: 89350838; PMID: 2764886
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GPPG 1035
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948 GIAGITGARGLAGPPGMPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTA 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 GAAGPPGPAAGTPGLQGMPGERGGLGSPGPKGDKGEPGGPGADGVPGKDGPRGPTGPI 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GV---MGFPGPKGAAGEPGKAGERGVPGP-------PGAVGPAGKDGEA 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 GPPGENGKPGEPGPKGDAGAPGAPGKGDAGAPGERGPPGLAGAPGLRGGAGPPGFEGK
                                                                        GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAA
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                                                                                                                                                 528 GVPGGPGMRGMPGSPGGPGSDGKPGPPGSQGESGRPGPPGPSGPRGQPGVMGFPGPKGND
                                                                                                                                                                                                                                                                                                                    588 GAPGKNGERGGPGGPPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTG
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A; Molecule type: mRNA
A; Residues: 165-1155, P., 1157-1466 «LOI>
A; Cross-references: EMBL, X0142; NID:g29584; PIDN:CAA25821.1
R; Miskulin, M.; Dalgleish, R.; Kluwe-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
Biochemistry 25, 1408-1413, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type
A; Accession: 15293; MUID:86187604; PMID:3754462
A; Residues: 1161-1200
A; Residues: 1162-1196
A; Residues: 1165-1196
A; Residues: 1
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Althoraxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently C (Genetics COL)
Althorax 2012A1
Althorax 2017, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2071, 94/3, 11/3, 149/3, 176/3, 554/3, 587/3, 1175/3, 1175/3, 1275/1, 1337/3, 1418/3
Althorax 2018 Althorax 2018 Althorax 2019 Althorax 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ation C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit 3-hydroxylated and some are subsequently
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Pred. No. 2.7e-86;
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Matches 365;
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end
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                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: COL3A1 Collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology F;30-90/Domain: von Willebrand factor type C repeat homology < VWC>
      Cyspecies: Gallus quillus (chicken)
Cyspecies: Gallus quillus (chicken)
Cyspecies: Gallus quillus (chicken)
Cyspecies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
CyAccession: 150694
R;Nah, H.D.; Niu, Z.; Adams, S.L.
J. Biol. Chem. 269, 16443-16448, 1994
A;Title: An alternative transcript of the chick type III collagen gene that does not alternative transcript of the Chick type III collagen gene that does not alternative translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                        A;Residues: 1-886 <NAH>
A;Cross-references: UNIPROT:P12105; EMBL:U07973; NID:g520454; PIDN:AAA83407.1; C;Genetics:
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chicken (fragment)
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nes 362; Conservative
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Best Local Simil
Matches 362; C
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GSPGEPGANGLPGAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPGRD 527

1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP

9

Indels 108;

209;

Mismatches

42;

Conservative

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GQDGR----PGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP---PGAVGPA 549
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                                                                                                                                                                                                                                                                                                271 GAKGLTGSPGSPGPDGKTGPPGPAGDDGRPGPPGARGQAGVMGPPGPKGAAGEPGKA 330
                                                                                                                                                                                                                                                                                                                391 GKPGEQGVPGDLGAPGPSGP-----AGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK 444
                                                                                                                                                                                                                                                                                                                                                                                                                 79 GPDGKTGPPGPAGQDGRPGPPGARGQ-----AGVMGFPGPKGAAGEPGKAGERGVP 132
                                                                                                              173 GFPGPPGPPGPPGHAGPPGSNGYQGPPGBPGQPGPSGPPGPAGMIGPAGPPGKDGEP 232
                                               -----GEAGLPGAKGLTGSPGSP 78
                                                                      233 GRÞGRNGDRGIÞGIÞGHKGHÞGMPGMPGMKGARGFDGKDGAKGDSGAÞGÞKGEAGQÞGAN
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1 GPPGEPGPTGLPGPPGERGGPGSRGF---PGADGVAGPKGPAGERGSPGPKGSPGEA
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P02452 homo sapien
O76045 homo sapien
Q8n473 homo sapien
Q9xsj7 canis famil
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P02457 gallus gall

099251 rana catesb

0802b5 xenopus lae

0802b5 xenopus lae

091654 rattus norv

091b91 xenopus norv

091b91 xenopus lae

014046 homo sapien

077753 canis famil

028396 equus caball

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000437 gallus gall

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1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 617
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Q810j9
Q6pcl3
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                    1825181 segs, 575374646 residues
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CA11 CHICK
Q9YIB4
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Q90W37
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Q6LAN8
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CA11_MOUSE
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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| Q910c0 oncorhynchu | 091000     | ~ | 1449 | 53.7 | 1873   | 45 |
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| P12105 gallus gall | CA13_CHICK | П | 1262 | 53.7 | 1873   | 44 |
| Q91718 xenopus lae | 091718     | ~ | 1491 | 53.9 | 1880   | 43 |
| Q7ztm4 xenopus lae | Q7ZTM4     | 7 | 1491 | 53.9 | 1880   | 42 |
| Q9w7r9 cynops pyrr | Q9W7R9     | 7 | 1418 | 54.0 | 1883   | 41 |
| Q7zti6 xenopus lae | Q7ZTI6     | N | 1486 | 54.1 | 1888.5 | 40 |
| Q91717 xenopus lae | 091717     | N | 1486 | 54.2 | 1890.5 | 39 |
| Aah63191 xenopus t | AAH63191   | ~ | 1492 | 54.2 | 1892   | 38 |
| Q6p4z2 xenopus tro | Q6P4Z2     | Ņ | 1492 | 54.2 | 1892   | 37 |
| P02453 bos taurus  | CA11_BOVIN | Н | 779  | 54.4 | 1898   | 36 |
| Aah63249 brachydan | AAH63249   | 0 | 1447 | 54.9 | 1914   | 35 |
| Q6p4ul brachydanio | Q6P4U1     | N | 1447 | 54.9 | 1914   | 34 |
| Q63123 rattus norv | Q63123     | ~ | 1419 | 55.1 | 1921   | 33 |
| Aar24536 brachydan | AAR24536   | 8 | 1447 | 55.1 | 1923   | 32 |
|                    |            |   |      |      |        |    |

### ALIGNMENTS

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Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockup D.J., "Structure of a full-length cDNA clone for the prepro alpha 1(I) chain of human type I procollagen."; Blochem. J. 253:919-922 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Click E.M., Bornstein P.; and and characterization of the cyanogen bromide peptides from "Isolation and characterization of the cyanogen bromide peptides from the alpha 1 and alpha 2 chains of human skin collagen.", Biochemistry 9:4699-4706(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-181 FROM N.A. EDDING-6462200; MINELLINES-84370697; PubMed-6462200; Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M., Myers J., Williams C., Ramirez F.; Myers J., Williams C., Ramirez F.; Chi Myers J., Williams C., Ramirez F.; Chi Myers J., Williams C., Ramirez F.; Annean proc alpha 1(1) collagen gene structure reveals evolutionary conservation of a pattern of introns and exons."; Nature 310:337-340(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=2843432;
D'Alessio M., Bernard M.P., Pretorius P.J., de Wet W., Ramirez F.,
Pretorious P.J.;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                             Q14992; Q15176;
Q9UMM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete nucleotide sequence of the region encompassing the twenty-five exons of the human pro alpha 1(1) collagen gene (COLIA1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dalgleish R.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 162-301, AND PYRROLIDONE CARBOXYLIC ACID
                                                            CA11 HUMAN STANDARD; PRT; 1464 AA. P02452; P78441; Q13895; Q13902; Q13903; Q14037; Q15010; Q16050; Q7K234; Q7K234; Q8IVIS; Q9UMLG; Q1-701-1966 (Rel. 01, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) NameleGen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANT SER-1434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-472 FROM N.A. MEDLINE=89025644; PubMed=3178743;
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RESULT 1
                                                                                 HID DESCRIPTION OF SELECTION OF
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SEQUENCE OF 425-1464 FROM N.A. MEDLINE=84080385; PubMed=6689127;

Q80X38 Q6U1J5

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PubMed=3857621;
Barsh G.S., Roush C.L., Bonadio J., Byers P.H., Gelinas R.E.;
"Intron-mediated recombination may cause a deletion in an alpha 1 type I collagen chain in a lethal form of osteogenesis imperfecta.";
Proc. Natl. Acad. Sci. U.S.A. 82:2870-2874 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1179-1464 FROM N.A., VARIANTS OI-II HIS-1277, ARG-1388 AND 1337-GLU-TYR-1338 DEL, AND VARIANT SER-1434.

MEDLINE-9335-2646; PubMed-8349697,
Chesalar S.D., Wallis G.A., Byers P.H.,
"Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I)
chain of type I collagen result in defective chain association and produce lethal osteogenesis imperfecta.";

Biol. Chem. 268:18218-18225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88097389; PubMed=3480516;
Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
"Regulatory elements in the first intron contribute to transcriptional control of the human alpha 1(1) collagen gene.";
Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=71001508; PubMed=4119110; Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.; Morgan P.H., Jacobs H.G., Seprest J.P., Cunningham L.W.; "A comparative study of glycopeptides derived from selected vertebrate
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F., Prockop D.J.;
"Nucleotide sequences of complementary deoxyribonucleic acids for the pro alpha 1 chain of human type I procollagen. Statistical evaluation of structures that are conserved during evolution.";
Biochemistry 22:5213-5223(1983).
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Muller P.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85130970; PubMed=2857713;
Chu M.-L., de Wet W., Bernard M.P., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
Promoter structure, Alul repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     critical crosslink region in human-bone-derived collagen type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maekelae J.K., Raassina M., Virta A., Vuorio E.,
"Human pro alpha 1(1) collagen: cDNA sequence for the C-propeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88033098; PubMed=2822714;
Rossouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez
                                                                                                                                                                                                                                                  Chu M.-L., Gargiulo V., Williams C.J., Ramirez F.;
"Multiexon deletion in an osteogenesis imperfecta variant with
increased type III collagen mRNA.";
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Eur. J. Biochem. 192:153-159(1990).
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                                                                                                                                                                                                                              PubMed=2981843;
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Wallis G.A., Starman B.J., Zinn A.B., Byers P.H.,
"Variable expression of osteogenesis imperfecta in a nuclear family is
explained by somatic mesaicism for a lethal point mutation in the
alpha 1(1) gene (COLIAN) of type I collagen in a parent.";
Am. J. Hum. Genet. 46:1034-1040(1990).
                                                                                                                                                                                                  Labhard M.E., Hollister D.W.;
"Segmental amplification of the entire helical and telopeptide regions of the cDNA for human alpha 1 (1) collagen.";
Matrix 10:124-130(1990).
collagens. A possible role of the carbohydrate in fibril formation.";
J. Biol. Chem. 245:5042-5048(1970).
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MEDIATE-91184577; bubmed=2010058;
Kilvaniemi H., Tromp G., Prockop D.J.;
"Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=83064528; PubMed=6183642;
Chu M.-L., Myers J.C., Bernard M.P., Ding J.-F., Ramirez F.;
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the human pro alpha 1[1] collagen chain.";
Nucleic Acids Res. 10:5925-5934(1982).
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MEDILINE-38181161; PubMed=7881420;
Forlino A., Zolezzi F., Valli M., Pignatti P.F., Cetta G.,
Brunelli P.C., Motres M.;
Brunelli P.C., Motres M.;
Brunelli P.C., Motres M.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1440-1464 FROM N.A.
MEDLINE=90110490; PubMed=2295701;
Willing M.C., Cohn D.H., Byers P.H.;
"Frameshift mutation near the 3' end of the COLIA1 gene of type collagen predicts an elongated Pro alpha 1(I) chain and results
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 425-490; 965-1024; 999-1039 AND 1453-1464 FROM N.A.
                                                                                                       SEQÜENCE OF 281-302; 402-420; 823-842; 924-944; 1026-1045 AND
1143-1162 FROM N.A.
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PubMed=3170557;
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J. Clin. Invest. 85:282-290(1990).
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FASEB J. 5:2052-2060(1991).
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                                                  Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
Promoter structure, Alul repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
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Korkko J.M., Earley J.J., Nuytinck L., DePaepe A., Prockop D.J.,
Ala-Kokko J.M.,
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF017178; AAB94054.2; -.
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005537; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR001007; VWF_C.
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SEQUENCE FROM N.A.
MEDLINE=89025644; PubMed=3178743;
Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
Jaenisch R., Prockop D.J.;
Structure of a full-length cDNA clone for the prepro alpha 1(1) of human type I procollagen.";
Biochem. J. 253:919-922(1988).
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MEDLINE=88329734; PubMed=2843432;
D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F.
"Complete nucleotide sequence of the region encompassing the fit
twenty-five exons of the human pro alpha 1(1) collagen gene.",
Gene 67:105-115(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91138770; PubMed=1995349;
Matta A., Bornstein P., Penttinen R.P.;
"Highly conserved sequences in the 3'-untranslated COLIA1 gene bind cell specific nuclear proteins.";
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Pfam: PF01410; COLF; 1.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD002078; Fib_collagen_C;
SMART; SM0018; COLF; 1.
PROSITE; PS01208; WMC 1; 1.
PROSITE; PS01208; WMC 1; 1.
                     SEQUENCE FROM N.A.
MEDLINE=85130970; Pubmed=2857713;
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   1118 GPPGPPGSPGEQGPSGASGPAGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1177
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                                                         Length 1464;
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Catarrhini; Hominidae;
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Last annotation update)
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                                                     64.1%; Score 2237.5; DB 1; 60.2%; Pred. No. 9.5e-83; ive 23; Mismatches 152;
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REVIEW ON OI VARIANTS.
MEDLINE=91374476; PubMed=1895312;
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Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
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O76045 01-NOV-1998 (TERBILTEL 12, L
01-NOV-1999 (TERBILTEL 12, L
01-NAR-2004 (TERBILTEL 26, L
Pro alpha 1(1) collagen.
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Best Local Similarity 60.23
Matches 441; Conservative
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OCCUPATION

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139010 MW;
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                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences.
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SMART; SM00214; VWC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad.
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                                                                                                                                                                                                                            GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GE-----AGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            755 GKDGVRGLTGPIGPPGPAGAPGDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPP 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                               935 GADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPP 994
                                                            48
                                                                                                                                                                          GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGPPGAGQA
                                                                                                                                                                                                                                                            GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAQGPPGPAGPAGERGEQGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGPAGEEGKRGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
                                                                                                                                            GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
                                                                                                                                                                                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----
                                                                                                                                                                                                                                                                                                                                                GSPGFPGLPGPAGPPGBAGKPGBQGVPGDLGAPGPSGARGBRGFPGBRGVQGPPGPAGPR
                                                                                                                                                                                                                                                                                                                                                                                         --TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
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                                                            -----GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
VOBI_TaxID=9606;
                     117;
Pred. No. 1.4e-82;
3; Mismatches 153; Indels
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequenc)
01-MA-2004 (TrEMBLrel. 26, Last annotath
Alpha 1 type I collagen, preproprotein.
Name=COLIA1;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGPPGARGQ------
llarity 60.0%; Pr
Conservative 23;
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Best Local Similarity
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Expleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gab L., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 GPPGPAGEEGKKGARGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 517
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R GO; GO:0005531; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
R GO; GO:0006201; F:extracellular matrix structural constituent; IEA.
R InterPro; IPRO03161; Cig_helix.
R InterPro; IPRO03661; Collagen.
R InterPro; IPRO03695; Fib collagen.
R InterPro; IPRO03695; Fib collagen.
R InterPro; IPRO03007; VWFC.
R Pfam; PFO1410; COLFT; 1.
R Pfam; PFO1410; COLFT; 1.
R Pfam; PFO1410; Collagen; 18.
R ProDom; PD000007; Cig_helix; 3.
R ProDom; PD000078; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 GPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001085; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
Pfam, PF01410; COLF1; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 2.
ProDom; PD002078; Fib_collagen_C; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS50184; VWFC_2; 1.
Collagen; Connective Lissue; Disease m
                                                                         Collagen, Connective tissue;
Glycoprotein; Hydroxylation;
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1460 AA; 138762
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les 441; Conservative
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                                                                  GAAGRVGPPGPSGNAGPPGPPGPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                     GEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP
                                                                                               GPAGP----KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                              GADGOPGAKGEPGDAGAKGDAGPPGPAGPAGPPGF1GNVGAPGAKGARGSAGPPGATGFP
                                                ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                               GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE-
                                                                                                                                                                                                                                                                                                                       30-MAY.2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A., AND VARIANT OI ALA-208
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
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                                                                                                                                                                                                                               Vonelical region (N-terminal).
Triple-helical region (C-terminal).
Nonhelical region (C-terminal).
Cell attachment site (Potential).
Cell attachment site (Potential).
Pyrrolidone carboxylic acid (By similarity).
Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxylysine (By similarity).
O-linked (Gal. . ) (By similarity).
O-linked (Gal. . ) (By similarity).
G-> A (in O1; severe).
G-> A (in O1; severe).
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Disease mutation; Extracellular matrix; Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.0%; Score 2231.5; DB 1; Length 1460; 60.2%; Pred. No. 1.7e-82; ive 20; Mismatches 155; Indels 117;
                                                                                           By similarity.
N-terminal propeptide.
Collagen alpha 1(1) chain.
C-terminal propeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
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NAT. Genet. 15:95-98(1997).

NON. TER. 1069 1069
                                                                                                                                                                                          479 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                   214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
                                                                                                                                                                                                                                                                                                         539 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER
                                                                      GPPGEAGKPGEOGVPGDLGAP-----GPPGPT
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57.6%; Pred. No. 3.3e-82;
ive 17; Mismatches 151; Indels 162; Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
collagen type I alpha 1 (Fragment).
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02-MAR-2004 (
02-MAR-2004 (
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                                                                                        .054 GPAGKNGDRGETGPAGPAGPIGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQ 1113
                                                                                                                                                                                        1114 GPPGPPGSPGEQGPSGASGPAGPRGPPGSAGSPGKDGLNGLPGPIGPPGPRGRTGDAGPV 1173
  994 GPMGPPGLAGPPGESGREGSPGAEGSPGRDGSPGPKGDRGETGPAGPPGAPGAPGAV 1053
                                                                                                                                             -AGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97141927; PubMed=8988177;
Simon M., Pedeutour F., O'Srien K., Sirvent N., Kedra D., Guilbaud C
Simon M., Pedeutour F., O'Brien K., Sirvent M., Kedra D., Guilbaud C
Turc-Carel C., Dannanski J.P.;
"Regulation of the platelet-derived growth factor B-chain gene via
fusion with collagen gene COLIAI in dermatofibrosarcoma protuberans
and giant-cell fibroblastoma.";
Nat. Genet. 15:95-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.7%; Score 2222; DB 2; Length 1069;
llarity 57.6%; Pred. No. 3.3e-82;
Conservative 17; Mismatches 151; Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A SEQUENCE FROM N.A.
A O'Brien K.P.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
B RMBL; X98705; CAA67261.1;
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR008161; Collagen.
InterPro; IPR009041; PMP_GCI.
InterPro; IPR009041; PMP_GCI.
InterPro; IPR001007; VMF_C.
InterPro; IPR001007; UMF_C.
InterPro; IPR001007; Clg helix; 3.
Pfam; PF001391; Collagen; 15.
Pfam; PF001391; Clg helix; 3.
R SMART; SM00214; VWC; I.
R PROSITE; PS00184; VWFC_1; 1.
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                                               GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update) .
Last annotation update)
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                                                                                                                                                                                                                                                                                  1174 GPPGPPGPPGPPG 1186
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                                                                                                                                          GPPGP----
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Best Local Similarity
Matches 448; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                             117 GPPĞQDGIPĞQPĞLPĞPPĞPPĞPLĞLGĞNFASQMSYGYDBKSAGVSVPĞPMĞPSĞPR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GLPGPPGAPGPQGFQGPPGEPGEPGGSGPMGPPGPPGPPGKNGDDGEAGKPGRPGERGPP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 gpogardiperadipemkehrefsgingakedifepadpkespespespergipegomeprelp 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GERGRPGPPGTAGARGNDGAVGAAGPPGPTGPTGPPGFPGAAGAKGEAGPQGARGSEGPQ
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1453 AA; 137886 MW; E6896BDC19A4A1D8
                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                              Query Match 63.5%; Score 2215.5; DB 2; Best Local Similarity 53.8%; Pred. No. 7.2e-82; Matches 446; Conservative 21; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                  1 GPPGE---PGPTGLPGPPGERGGPGSRGFPG---
GO; GO:0006817; P:phosphate transport;
        InterPro; IPR00816; Clg Helix.
InterPro; IPR00816; Collagen.
InterPro; IPR00816; Collagen.
InterPro; IPR009085; Fib Collagen.
InterPro; IPR001007; WWF.C.
Pfam; PF01410; Collagen; 18.
ProDom; PP00207; Clg Helix; 3.
ProDom; PD000007; Clg Helix; 3.
ProDom; PD000007; Clg Helix; 3.
ProDom; PD000007; Clg Helix; 3.
ProDom; PD002008; Colf i 1.
PR0SITE; PS01208; WWFC 1; 1.
PR0SITE; PS01208; WWFC 1; 1.
PR0SITE; PS01208; WWFC 1; 1.
PR0SITE; PS01208; WWFC 2; 1.
Collagen.
INOW TER 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            839 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 898
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MEDLINE=99163824; PubMed10065941;
MEDLINE=99163824; PubMed10065941;
Expression of collagen alphal(I) mRNA variants during tooth and bone formation in the rat.";

formation in the rat.";

EMBL: Res. 78:11-19(1999).

EMBL: Z78279; CAB016331; -...

GO: 000505737; C:cytoplasm; IEA.

GO: GO:0005737; C:cytoplasm; IEA.

GO: GO:0005737; C:cytoplasm; IEA.

GO: GO:0005737; C:cytoplasm; IEA.
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                                                                                          603079;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NIV-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Collagen alphal (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL TaxID=10116;
                                                                   GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA----
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 GRPGEAGLP - - GAKGLTGSPGSPGP-
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213 -----TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSP
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AAA37332.1; JOINED.
AAA37332.1; JOINED.
AAA37332.1; JOINED.
AAA37332.1; JOINED.
                                               AAA37334.1;
CAA29927.1;
AAA37332.1;
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AAA37332.1;
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K03035;
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K03036;
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K03032;
                                     M14423;
                                               M17491;
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                         X15896;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-88124276; PubMed=3340560,
MEDLINE-88124276; PubMed=3340560,
MEDLINE-88124276; PubMed=3340560,
"Two mRNAs of mouse pro alpha 1(1) collagen gene differ in the size of the 3'-untranslated region.";
Mucleic Acids Res. 16:773-773(1988).
-! FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-! SUBULIT: Triners of one alpha 2(1) and two alpha 1(1) chains.
-! TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86137403; PubMed=3841523;
French B.T., Lee W.-H., Maul G.G.;
"Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I) collagen
                                                                                                                                                                                                                                                                           MEDLINE=96033240; PubMed=8535610;
Li S. W., Khillan J., Prockop D.J.;
"The complete cDMA coding sequence for the mouse pro alpha 1(I) chain
of type I procollagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 735-1130 FROM N.A.
MEDLINE=83141374; PubMed=6298597;
Monson J.M., Friedman J., McCarthy B.J.;
"DNA, sequence analysis of a mouse pro alpha 1 (1) procollagen gene: evidence for a mouse B1 element within the gene.";
Mol. Cell. Biol. 2:1362-1371(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTW: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 WWFC domain.
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
MEDLINE-83157109; PubMed-6219867;
Monson J.M., McCarthy B.J.;
"Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
evidence for insertions or deletions in gene coding sequences.";
DNA 1:59-69(1981).
         568 GERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 616
                                897 GPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGSPGTPGPQGIAG 945
                                                                                                      01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                 PRT; 1453 AA
                                                                                                                                                                                                                                                                                                                               Matrix Biol. 14:593-595 (1995).
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 518-1128 FROM N.A.
                                                                                                                                                                         Name=Collal; Synonyms=Colal;
Mus musculus (Mouse).
                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydroxyapatite.
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                                                                                                                                                                                                                                                                  STRAIN=FVB/N
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Allyaine (By similarity).

5-hydroxylysine (By similarity).

3-hydroxyproline (By similarity).

N-linked (GlonAc. ) (Potential).

N-linked (GalonAc. ) (By similarity).

N-linked (GalonAc. ) (By similarity).

Cell attachment site (Potential).

A -> v (in Ref. 5).
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REPERSONAL STATES STATE
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Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal propeptide.
Collagen alpha 1(I) chain.
C-terminal propeptide.
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987 GPMGPPGLAGPPGESGREGSPGAEGSPGRDGAPGAKGDRGETGPAGPPGAPGAPGAPGAPGPV 1046
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                                                    Strainsberg R.

EMBL; BC050014 AAH50014.1; -.

R MGD; MG1:88467; Colla1.

R GO; GO:0005581; C:cytolasm; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR0008161; Clg helix.

R InterPro; IPR0008161; Clg helix.

R InterPro; IPR0008041; PMP_SGCI.

R InterPro; IPR0009041; PMP_SGCI.

R InterPro; IPR0009041; PMP_SGCI.

R Ffam; PF01191; COLFI: 1.

R Ffam; PF001391; COLFI: 1.

R ProDom; PD000077; Clg helix: 3.

R ProDom; PD000077; Clg helix: 3.

R ProDom; PD000078; Fib_collagen_C: 1.

R SMART; SM00214; VWC: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687 GNNGAPGNDGAKGDTGAPGAPGAGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSP
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[2]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collagen.
SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE—colon;

X Strausberg R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L.; Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.D.; Colling F.S.; Wagner L., Shenmen C.M.; Schuler G.D.,

A Stagheron M. Bare N.B. Buetow K.H., Schaefer C.F., Bhare N.K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stagheron M., Soares M.B., Bonaldo M.F.; Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Tooshiyuki S., Carrinci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcian A.M., Gay L.J., Hulyk S.W.,

Yillaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcianes S., Sanchez A.,

Whiting M., Madan A., Young A.C., Sheychenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Sheychenko Y., Boulfard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K Rzzyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Dones S.J., Marx M.A.,

""" Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                      GADGOPGAKGEPGDTGVKGDAGPPGPAGPPGPIGNVGAPGPKGPKGPRGAAGPPGATGFP 866
                                                                                                                                                                                                                             ----VGPAGKDGEAGAQGPPGPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                            GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP 453
  GNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMPGERGAAGLPGPKGDKGDAGPKGADGSP
                                                                                                                                                                                                                                                                                                                                                      GADGPAGSPGTPGPQGTAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGPSGSSGERGPP
                                                                                                                                                                                                                                                                                                                                                                                                GPAGP---KGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVP
                                                               ---AGRPGEAGLPGAKGLTGSPGSPGPD-----GKTGPPGPAGQDGRP
                                                                                                     GKDGARGLTGPIGPPGPAGAPGDKGEAGPSGPPGPTGARGAPGDRGEAGPPGPAGPP
                                                                                                                                                                                                                                                                     GAAGRVGPPGPPGPPGPVGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSP
                                                                                                                                                   --AGVMGFPGPKGAAGEPGKAGERGVPGPPGA----
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Sciurognathi, Muridae, Murinae, Mus
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0810009;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GARGOAGVMGFPGPKGAAGEPGKAGERGVPGP-----
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLGAPGPSGPAG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequences.
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                                                                                                                                                   GPPGPPGARGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Collal;
Mus musculus
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117860 MW; B6B86CBB4457F4D9 CRC64;
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Collal protein.
                                                                                                                                             49 GPKGSPGEAGRP-
     1225 AA;
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SEQUENCE FROM N.A.
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     SEQUENCE
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TISSUE-Mammary tunnor. WAP-TGF alpha model. 7 months old;

MEDLINE-22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Datchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

B Datchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

B Tomnstein M.J., Uodin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Albards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Halp J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Nitlang M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

R Nitlang M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

R Richeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R Richeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R Richeley R.W., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                            547 GPAGKDGBAGAPGPPGPAGBRGEQGPAGSP---GFQGLPGPAGPPGBAGKPGEQGVP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (CT-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC059281; AAH59281.1;

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Claden.

InterPro; IPR008185; Fib collagen.

InterPro; IPR008985; Fib collagen.

InterPro; IPR008985; Fib collagen.

InterPro; IPR001007; WWF.C.

InterPro; IPR001007; WWF.C.

InterPro; IPR001007; WWF.C.

InterPro; IPR001007; VWF.C.

InterPro; IPR001007; Clg helix; 2.

IPR0Dom; PD002078; Fib collagen.C; 1.

SMART; SM00214; VWC; 1.
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TISSUE-Mammary tumor, WAP-TGF alpha model, 7 months old;
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                  1225 AA
                                                                                                                                                                                                                            Created)
                                                                                                                             1167 GPPGPPGPPGPPG 1179
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                                                                                                 604 GDLGAPGPSGPAG 616
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Collal protein.
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                               Name=Collal;
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                                                                                                                                                                                                                                                                                                                                                                                        94 GRPGPPGPPGARGQAGVMGFPGPKGAAGE-----PGKAGERGVPGPPGAVGPAGKDGEA
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                                                                                                                                      1 GPPGEPGPTGLPGPPGE------RGGPGSRGFPGADGVAGPKGPAGERGSPGPA
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                                                                         144; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
      62.4%; Score 2176.5; DB 2; Length 1225; 56.7%; Pred. No. 2.4e-80; ive 28; Mismatches 157; Indels 144;
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Last sequence update)
Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
Query Match
Best Local Similarity 56.7%
Matches 431, Conservative
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NCBI_TaxID=9031;
                                                                                                                                                                                                                        CHICK
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       487
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ID CA11_CHI
AC P02457;
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   MEDIANE-22388257; PubMed=1247732;

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Botchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Branctein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Bhiting M., Madan A., Young A.C., Shackochenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Manner A.N.,

A Maria M.A.;

A Maria M.A.;

A Maria M.A.;

A Goberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239
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                                                                                                                                                                                                                                                                                                                                                      Stransberg R.; Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC059281; AAH59281.1; -. SEQUENCE 1225 AA; 117860 NW; BCB86CBB4457F4D9 CRC64;
                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary tumor;
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Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              431; Conservative
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MEDLINE=82231995; PubMed=7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.,
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MEDLINE=72243016; PubMed=5047697;
Byre D.R., Glincher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
GPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV
                                                                      GPAGKDGEAGAQGPPGPAGPAGERGE-------QGPAGSPGFQGLPGPA----
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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MEDLINE=88056316; PubMed=3678834;
Finer M.H., Boedtker H., Doty P.,
"Construction and characterization of cDNA clones encoding the 5'
of the chicken pro alpha I(I) collagen mRNA.";
Gene 56:71-78(1987).
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MEDLINE=80134546; PubMed=6987088;
Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T.,
Pastan I., Decrombrughbe B., Fietzek P.P., Olsen B.R.;
"Nucleotide sequence of a collagen co
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MEDLINE-88007542; PubMed=2820966;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., and S. Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., and S. Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., Ano S., Gerstenfeld L.C., Boedtker H., Finer M., Finer
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(I) chain precursor.
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MEDLINE=81160715; PubMed=6927845;
Fuller F., Boedtker H.;
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987 GPMGPPGLAGPPGEAGREGAPGAEGAPGRDGAAGPKGDRGETGPAGPPGAPGAPGAPGPV 1046
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                                                                                                                                         GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP----
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                                                                                        567 GVMGFPGPKGAAGEPGKPGERGAPGPPGAVGAAGKDGEAGAQGPPGPTGPAGERGEQGPA
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GO: GO: 0005581; C: collagen; IEA.
GO: GO: 0005581; C: collagen; IEA.
GO: GO: 0005201; F: extracollular matrix structural constituent; IEA.
GO: GO: 0006817; P: phosphate transport; IEA.
InterPro; IPR008161; Clg_helix.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
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(TremBLrel. 10, Last sequence update)
(TremBLrel. 26, Last annotation update)
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NCBI_TaxID=8330;
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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|447 GPPGPAGEEGKRGÅRGEFGPAGLPGPAGERGAPGSRGFPGADGIAGPKGPPGERGSPGAV 506
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                 -i- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-i- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-i- TISSUE SPECIFICITY: Forms the fibrils of tendon, liquments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 Allysine Characteristics and Allysine (By similarity).
254 5-hydroxylysine (By similarity).
1081 Hydroxylysine (Potential).
1153 5-hydroxylysine (Potential).
1153 3-hydroxylysine (Potential).
254 O-linked (Gal.). (By similarity).
1187 F -> L in Ref. 5).
1187 P -> L in Ref. 5).
141 Q -> H (in Ref. 6).
A, 137789 Mw, 3BC6152134271F4D CRC64;
                                                                                                                                                       PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X. BIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.7%; Score 2151.5; DB 1; Length 1453;
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Extracellular matrix; Glycoprotein; Hydroxylation;
Pyrrolidone carboxylic acid; Repeat; Signal.
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Collagen alpha 1(I) cha
C-terminal propeptide.
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Interpro; IPR008160; Collagen.
Interpro; IPR008160; Collagen.
Interpro; IPR00100; VWFC.
Fan; PF04140; CoLFI; 1.
Fan; PF01391; Collagen; 18.
Ffan; PF01093; VWC; 1.
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ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M17839; AAA48704.1; -.
EMBL; M17838; AAA48704.1; JOINED.
EMBL; V00401; CAA23695.1; -.
EMBL; M17671; AAA48671.1; ALT_SEQ.
EMBL; M17671; AAA48672.1; -.
PIR; A27179; A27179.
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PROSITE; PS50184; VWFC_2; 1.
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                                                                                                                                                                                                                                                                                                                Indels 117; Gaps
                                                                                                                                                                                                                                                                      Query Match

58.6%; Score 2043.5; DB 2; Length 1450;
Best Local Similarity 54.7%; Pred. No. 5.7e-75;
Matches 401; Conservative 31; Mismatches 184; Indels 117;
                                                                                                                                                                                                                                     1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
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InterPro; IPR001007; VWF_C.
Pfam; PF01410; COLFI; 1.
Pfo.Don; PF001391; Collagen: 18.
ProDom; PD00007; Clagen: 18.
ProDom; P0002078; Fib_collagen_C; 1.
SWART; SW0018; Fib_collagen_C; 1.
PROSITE; P801208; VWFC_1; 1.
PROSITE; P851208; VWFC_1; 1.
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74

RESULT 093251

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18;
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                                                                                                                                                                                                                                                                                        WEDURNER FYON N.W.
Asahina K., Utoh R., Obara M., Yoshizato K.;
Asahina K., Utoh R., Obara M., Yoshizato K.;
Asahina K., Utoh R., Obara M., Yoshizato K.;
Tof cell-type specific and thyroid hormone-dependent expression of genes
of al(I) and al(I) collagen in intestine duting
amphibianmetamorphosis.";
Matrix Biol. 18:89-103(1999).
EMBL; ABOIL440; BB-103(1999).
EMBL; ABOIL440; BB-103(1999).
GO; GO:0005591; C:collagen; IEA.
GO; GO:0005501; C:cytoplase, IEA.
GO; GO:0005501; F:extracellular matrix structural constituent, IEA.
GO; GO:0005501; F:extracellular matrix
GO; GO:0005801; F:extracellular matrix
EMBL; PRO08861; C:collagen. C.
InterPro; IPR008861; Collagen.
InterPro; IPR008861; Collagen.
InterPro; IPR001895; Fib_collagen. C.
InterPro; GO:000501; Collagen. 18.
From, PP0110; Coller: 11.
SRART; SM00189; Collagen. C; 1.
SRART; SM00189; COLPI; 1.
SRART; SM00149; VWC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPQGSRGPDGPQGARGEPGAPGQAGPAGSAGNPGTDGQPGAKGATGAPGIAGAPGFPGAR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 GAPGPQGPGGSPGPKGNNGEPGAQGNKGEPGAKGESGPAGSQGPPGPPGEEGKRGSRGEP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 GKPGRPGERGPPGPQGARGLPGTAGLPGMKGHRGPNGLDGAKGDTGPAGPKGEPGNPGEN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 GODGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                          Alpha I type I collagen.
Name-alpha I type I collagen;
Rama catesbeiana (Bull Torana).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

58.6%; Score 2042.5; DB 2; Length

Best Local Similarity 49.7%; Pred. No. 6.2e-75;

Matches 421; Conservative 34; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGEPGPTGLPGPPGERGGPGS-----RGFPGADGVAGPKGPA
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137251 MW;
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PROSITE; PS50184; VWFC 2; 1.
   01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKPGEOGVPGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1445 AA;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=8400;
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1449 AA; 137464 MW;
                                                      Dev. Dyn. 225:384-391(2002)
                                                                                        FROM N.A.
     Richardson P.;
                                                                                                              TISSUE=Embryo;
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A NEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Antausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Brangeton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., A. Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., A. Flaton B.K., Kurzhy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B.K., Kurzhy D.M., Gaergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B.K., Kortenan M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Brainwar A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S., W. Jones S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Schner B.D., Schner B.D.
                                                                                                                                                                                                                                                                                                                                                           941 GTRGTVGLPGQRGERGFPGLPGPTGEPGKQGSSGPSGBRGPPGPGPPGEPGRE 1000
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                                                                                                                                                                                     495
                                                                         760
                                                                                                                                                                                                                        880
                                                                                                                                                                                                                                                                                          881 GPSGPAGKEGOKGPRGETGPAGRPGEPGAAGPPGPSGEKGSPGSDGPAGAPGIPGPQGIA 940
                                                                                                                                                                                                                                                                                                                                ----- 563
                                                                                                                                   GKPGEQGAPGDVGPSGPAGSRGERGFPGERGAIGPPGPQGPRGANGAPGNDGAKGEAGAP
                                                                   701 GAPGGQGPSGLQGMPGERGAGGLPGAKGDRGDQGPKGADGAPGKDGVRGLTGPIGPPGPG
                                                                                                              -- KGSPGEAGRP
                                                                                                                                                                                   -GSPGPDGKTGPP
                                                                                                                                                                                                                    821 GDAGPPGAAGPTGAPGPAGAVGATGPKGARGPAGPPGSTGFPGAAGRVGPPGPSGNAGPP
                                                                                                                                                                                                                                                         -GPAGQDGRP---GPPGP-----PGARGQAGVMGFPGPKGAA
                                                                                                                                                                                                                                                                                                                                                                                                    564 ------AGPAGERGEQGPAGSPGFPGGLPGPAGPPGEAGKPGEQGVPGDLGAP
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MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                    ---GP-GSRGFPGADGV-
                                                                                                                                                                                                                                                                                                                             GE----AGKAGERGVPGPPGAVGPACKDGE---AGAQGPPGP
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                          -----GERGSPGPAGP
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                                                                                                                                                                                   GEAGLPGAKGLTGSP------
                                  -----GPTGLPGPPGERG-
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                                                                                                          -----AGPKGPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423
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                                                                                                                                                                                                Alein S., Strausberg R.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC04982929.14.

REMBL; BC04982929.14.

RO; GO:0005581; C:collagen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005137; C:cytoplasm; IEA.

RO; GO:0006817; P:phosphate transport; IEA.

RICEPPO; IPR008161; Cglagen.

RICEPPO; IPR008160; Collagen.

RICEPPO; IPR001060; WWF_C.

REPEND; PF01410; COLFI; 1.

REPRD; REPROSO SI SEL COLFI; 1.
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SMART; SM0038; COLFI; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
Collagen.
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October 18, 2004, 13:22:25; Search time 129.602 Seconds (without alignments) 2272.479 Million cell updates/sec
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database :

SUMMARIES

# Res

| Description         | Human r  | Human re | <u>۲</u> | 2535 Pc | 544 A human | 1403 Amino ac | 1540 Am  | 1538     | 3485 Human | 2029     | 5055 Human | Add45051 Human Pro | 3947 Human | 136 Human | 541 Amino ac | Aay84539 Amino aci | Aab82454 Human pro | 764 Human | 0        | 1471     | 7417     | Abr92064 Human cer | 1142 Human sr | 565246 | 9470 Human so |  |
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# ALIGNMENTS

Plasma substitute; Gelatin-like protein; plasma expander; human. Human recombinant gelatin-like polypeptide Hu-4. Example 1; SEQ ID NO 3; 31pp; English. ADM48392 standard; protein; 821 AA. 11-SEP-2002; 2002EP-00078745. 11-SEP-2002; 2002EP-00078745. (FUJF ) FUJI PHOTO FILM BV. (first entry) Bouwstra JB, Toda Y; WPI; 2004-229415/22. EP1398324-A1. Homo sapiens. 17-MAR-2004. 03-JUN-2004 ADM48392; ADM48392 

Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.

The present sequence is the protein sequence of recombinant gelatin-like protein Hu-3. This is a tetramer of human recombinant gelatin-like protein Hu-1 ADM48390. A claimed composition suitable as a substitute for protein Hu-1 ADM48390. A claimed composition suitable as a substitute for protein Hu-1 ADM48390. A claimed substitue a protein having a colloid cosmocite function. The protein is a recombinant gelatin-like protein with a molecular weight of at least 10 Kba and at most 50 Kba and an composition of a less than 8. It is especially Hu-1 or Hu-deam composition of less than 8. It is especially Hu-1 or Hu-deam ADM48393. The recombinant gelatin-like protein, or a dimer, trimer or clearance rate from blood circulation, provides better and predictable corregulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin derivatives. Recombinant gelatin-correct of the proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to

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pharmaceutically active compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the interstitum. Clearance by liver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotting, vasodilation, function of exythrocytes, thrombocytes and leukocytes, immune responses, and blood levels of messenger molecules such as
                                                                                                                                                                                                                                                       1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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ive 0; Mismatches 0;
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The present sequence is the protein sequence of recombinant gelatin-like protein Hu-1 ADM48390. A claimed composition suitable as a substitute for plasma composition suitable as a substitute for plasma comprises a solution of saline and a protein having a colloid osmotic function. The protein is a recombinant gelatin-like protein with a colloid osmotic function. The protein is a recombinant gelatin-like protein with a combinant gelatin-like protein, or a dimer, trimer or tetramer of the recombinant gelatin-like protein, or a dimer, trimer or tetramer of the protein, is useful as a plasma expander that has a lower clearance rate from blood circulation, provides better and predictable regulation of clearance rate and which is less susceptible to proteolytic degradation than presently used gelatin-like proteins that are in essence free of hydroxyproline do not give rise to an immunological reaction with blood samples containing IgE antibodies. The gelatin-like proteins can be covalently attached to pharmaceutically cative compounds. After administration, the coupled medicament will not diffuse from the circulating blood into the intersitium. Clearance by cliver and kidney will be kept to a minimum, ensuring a more constant plasma level of the medicament. Suitable medicaments include those involved in intervening blood clotthing vasodilation, function of environment and leukocytes, immune responses, and blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful as substitute for plasma, comprises solution of saline and recombinant gelatin-like protein having colloid osmotic function.
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                                                                                                                                      Human recombinant gelatin-like polypeptide Hu-3.
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                ADM48391 standard; protein; 617 AA.
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100.0%; Pie.
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Les 616; Conservative
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                                                                                                                                                                                                                 Homo sapiens
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                                                                                               03-JUN-2004
                                                       ADM48391;
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culture support comprises the step of coating a microcarrier bead with comprises the protein having a molecular weight of about 40-
200 kba, and optionally further comprising the step of immobilising the comprete than 75%, preferably more than 85% and more preferably more than 95% of the gelatine-like protein on the microcarrier. In this process, contemplatine or gelatine-like protein has the same molecular weight. Contemplatine or gelatine-like protein is recombinantly produced to obtain a material of uniform molecular weight and to reduce the risk of contamination with prions. A claimed cell support consists of microbeads of 50.500 um size coated with a gelatine-like protein consisting of at least 95% Gly-xaa-yaa triplets and containing at least 15% proline residues and less than 5% of hydroxyproline residues, with a molecular weight distribution showing a maximum between 40 and 200 kpa, at least 75% of the protein molecules having a molecular weight within 2% of the maximum. Large-scale production of expressed products can be accomplished with gelatine-coated microcarriers.
                                                                                                                                                                                                                                                                           / Match 75.0%; Score 3482; DB 8; L Local Similarity 100.0%; Pred. No. 5.1e-207; Nes 616; Conservative 0; Mismatches 0;
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                                    GPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
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             GPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPK
                                                                    GPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP
                                                                                                                           GPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPA
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                                                                                                                     GEPGPPGPAGAAGPAGNPGADGQPGGKGANGAPGIAGAPGFPGARGPSGPPGPK
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                                                                                                                                                                                                                                                                   GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is porcine alphal(I) collagen. The present invention relates to recombinant synthesis of collagens and gelatins derived from animals. Collagen is useful in medical, pharmaceutical, food and cosmetic industries. Collagen is an important component of arterial sealants, bone grafts, drug delivery system, dermal implants, haemostats, and incontinence implants and for treating autoimmune disorders such as rheumatoid arthritis. Collagen is useful in food products such as sausage casings, and in cosmetics or facial and skin products such as sausage moisturisers. Recombinant gelatin is useful in vaccine formulations for treating viral infections, autoimmune diseases and cancer. Galatin is medical devices and products, in food and beverage industries, in hair medical devices and products, as a glue or adhesive in various manufacturing processes, as a light-sensitive costing in various and parterial partitive costing in various and elementary in the medical hase in which the care products, as a light sensitive costing in various
                                                                                                             Porcine, alphal(I) collagen; gelatin; cytostatic; viral infection; bharmaceutical; food industry; cosmetic; autoimmune disorder; vaccine; medical; arterial sealant; bone graft; dermal implant; haemostat; cancer; rheumatoid arthritis; beverage; photographic application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic devices, as photoregist base in photolithographic processes, in printing and photographic applications, in laboratory application, ar as a component in various gels used for biochemical and electrophoretic
                                                                                                                                                                                                                                                                                                       829. .830
/note= "Encoded by ggcgaacctggtgatgctggtgctaaaggcgatg
ctggtccccccggccctgctgga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated and purified bovine or porcine collagens and gelatins useful in medical, pharmaceutical, food and cosmetic industries, as vaccine, and for treating autoimmune disorders, infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGAPGPQGFQGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRPGERGPPGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 8; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polarek JW,
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                                                                  Porcine alpha1(I) collagen
                    (first entry)
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N-PSDB; AAD06576.
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                                                                                                                                                                                                                                                                                        Key
Misc-difference
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                    10-AUG-2001
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Matches
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Connolly

Zhang G,

Sequence 1057 AA;

19; GRPGEAGLP---GAKGLIGSPGSPGP-----DGKIGPPGPAGODGRPGPPGAR 105 150 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 197 -----AGSPGFOGLPGPA 180 GPRGSEGPQGVRGEPGPPGPAGPAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 257 ---GPSGPA-----GEPGPT 213 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 273 57 77 18 GPMGPSGPRGLPGPPGAPGPQGPPGBPGBPGASGPWGPPGPPGPPGRNGDDGBAGKP 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---GOAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ Gaps Query Match

59.6%; Score 2765; DB 3; Length 1057;

Best Local Similarity 55.4%; Pred. No. 1.1e-162;

Matches 561; Conservative 31; Mismatches 228; Indels 192; GPPGPAGPAGERGEQGP-------GPPGEAGKPGEQGVPGDLGAP-----28 78 901 138 151 198 181 258 214 В à g ò g ò 음 상 음 à

GVVGLPGQRGERGPPGLPGPSGEPGKQGPSGASGERGPPGPPGLAGPPGESGREGAP 857 735 977 393 497 423 678 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 737 562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618 738 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR 797 GXAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA 771 437 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 377 619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP----KGSPGEAGRPGEA GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFFGPRGAAGEPGKAGER GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 475 GAK-----GLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQ------516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP GEQGVPGDLGAPGPSGPAGE-----PGP-----PGP------TGLPGPP 424 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GPRGPPGSAGAPGKDGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPG 1029 GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG 820 798 919 772 318 378 334 438 394 274 g q ð 원 δ 음 ò g ò g ò જે à ò g ö g δ 셤

Ą AAY84403 standard; protein; 1058 (first entry) 12-JUL-2000 AAY84403;

Alphal collagen; 3,4-dehydro-L-proline; epoxidation; 3,4-epoxyproline; collagen; mussel adhesive protein; bloadhesive. Amino acid sequence of human type 1 (alphal) collagen polypeptide. WO200014201-A1 Homo sapiens 16-MAR-2000. RESULT 6
AAY84403
AAY84403
XX
AC AAY8
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DT 12-C
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ADD Amir
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PP
PD 16-P
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98US-0099652P US SURGICAL CORP. PAOLELLA D N. GRUSKIN E A. 09-SEP-1998; (USSU) 1 (PAOL/) 1 (GRUS/) (

99WO-US020462

07-SEP-1999;

738 618 798 675 858 771 978

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GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDA 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; decorin; ohimera.
                                                                                                                                                           GPAGP---AGERGEQGPAGSPGFOGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                                    679 GPPGPAGPAGPPGPIGNVGAPGAKGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                                               739 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                                                                                                                                                619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP----KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                      799 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP
                                                                                                                                                                                                                                                                                                                                                                                                                     919 GPAGARGPAGPOGPRGDKGETGEOGDRGIKGHRGFSGLOGPPGPPGSPGEOGPSGASGPA
                                                                                                                                                                                                                                                                                                          676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                                        -----AGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a chimeric collagen 1 (alphal)/decorin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of extracellular matrix proteins containing 4-trans-
hydroxyproline results in native self aggregating proteins, useful on
medical implants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
                                                                                                                                                                                                                                                                                                                                                                                  736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP---
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                                                                                 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Fig 18; 260pp; English
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N-PSDB; AAA12500.
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       475 GAK--
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                                                                                                                                                                                                                                      The present sequence represents a human type 1 (alphal) collagen protein of 3.4-deahdro-L-prolline into the peptide, using the method of the invention. The specification describes a method for the incorporation of non-natural amino acid into a polypeptide. The method comprises reacting the area of a least one 3.4-dehydroprolline residue in the polypeptide with an epoxydation reacted from a polypeptide containing at least one 3.4-dehydroprolline residue ontaining at least one 3.4-dehydroprolline residue. The method is used for studying the effects of non-natural amino acids on structure and function of polypeptides. The method is also useful for commercial production of collagen or mussel adhesive proteins (which are useful as bloadhesives), and for incorporating a wide variety of groups, including therapeutic ligands and biological probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 618
                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 GPQGPPGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEGKRGARGEPGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319. GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGPPGAVGPAGKDGBAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP
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                                                                                                                                     e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 192;
                                                                                                                               Incorporating non-natural amino acid into polypeptide, useful production of bloadhesives, by epoxidation or substitution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%; Score 2765; DB 3; 35.4%; Pred. No. 1.1e-162; ive 31; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEQGVPGDLGAPGPSGPAGE------PGP---
                                       Buechter DD;
                                                                                                                                                                                                      Disclosure; Fig 6; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGEAGKPGEOGVPGDLGAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGPAGPAGERGEOGP
                                 Paolella DN, Gruskin EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.43
Matches 561; Conservative
                                                                                                                                                 production of bioadhesivedehydroproline residues.
                                                                         WPI; 2000-271051/23.
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BUECHTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1058 AA;
                                                                                           N-PSDB; AAZ99843
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily depreciated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell, incorporating the nucleic acid sequence into the cell, and contacting the incorporating the nucleic acid sequence into the cell, and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated incorporated into the extracellular matrix protein. The content of mathod may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinagen and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proteins which do not normally contain trans-4-hydroxyproline. The present sequence represents a chimeric collagen I (alphal)/decorin protein, which may be produced using the method of the invention

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GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP

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GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP

675

619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA

738 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGOR

GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP------AGPA 771 918 GPAGARGPAGPPGGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGBQGPSGASGPA 977

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GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG

772

676 GLPGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGOAGVMGFPGPKGAAGBP

Sequence 1107 AA;

19; 105 150 180 213 317 273 333 GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAAGEPGKAGER 437 393 GEQGVPGDLGAPGPSGPAGE------PGP-----TGLPGPP 423 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP 474 617 137 197 257 57 77 214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GEOGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GAK------GLTGSPGSPGPDGKTGPPGPAGDDGRPGPPGARGQ-----GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---18 GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 106 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ ------AGSPGFOGLPGPA 198 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS GPPGEAGKPGEQGVPGDLGAP-----GEPGPT GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER Gaps 59.6%; Score 2765; DB 3; Length 1107; 55.4%; Pred. No. 1.2e-162; iive 31; Mismatches 228; Indels 192; GPPGPAGPAGERGEOGP-Local Similarity 55.49 475 151 181 258 318 274 378 334 438 394 498 424 558 618 50 Query Match Best Loca Matches 원 장 연 8 8 8 B 8 ò 셤 g à g à dd à 엄 ò g ò  $\stackrel{>}{\circ}$ 

----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP

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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; 6 encurerion of extracellular matrix proteins containing 4-trans-hydroxyproline results in native self aggregating proteins, useful medical implants. GPRGPPGSAGAPGKDGLNGLPGPPGPPGPRGRTGDAGPVGPPGPPGPPG 1029 A chimeric collagen 1 (alphal)/TGF-betal protein. ĸ, Connolly /note= "Gly encoded by GCT" Ö Ź Location/Qualifiers Claim 23; Fig 15; 260pp; English. Zhang AAY84538 standard; protein; 1171 99EP-00119184. 98US-00169768. (first entry) Buechter DD, (USSU ) US SURGICAL CORP. WPI; 2000-259138/23. N-PSDB; AAA12498 Key Misc-difference 07-OCT-1999; 09-OCT-1998; Homo sapiens Unidentified 25-JUL-2000 Gruskin EA, 12-APR-2000 EP992586-A2 AAY84538; 978 Chimeric AAY84538 

Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation; ss. transforming growth factor-betal; TGF-betal; chimera.

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-- KGSPGEAGRPGEA 675

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GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP-

519 198 9/9 828 38 918

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GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP

---AGAOGPPGP-----AGPA

GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGBQGPSGASGPA

GKAGERGVPGPPGAVGPAGKDGE--

GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG

978 772

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ద 8 AAW68485 standard; protein; 1464 AA.

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incorporating the nucleic acid sequence into the cell; and contacting the selected from the growth medium containing at least one amino acid, hydroxyproline and and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The hydroxyproline into proteins. This is especially useful in the hydroxyproline into proteins. This is especially useful in the ecombinant production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proline. The proteins depends on the post translational hydroxylation of proline. The polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence represents collagen 1 (alphal)/transforming sprott in translational hydroxylation of proline. The present sequence represents collagen 1 (alphal)/transforming sprott factor-betal (TGF-betal) protein, which may be produced using the marked is a two translation of proline may be produced using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1171 AA;
          8×6666666666666666888
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|   | 19;                   |
|---|-----------------------|
|   | gaps                  |
| .171;   | 192;                  |
| Length 1  | Indels 192; (         |
| )B 3;<br>-162;  | 228;                  |
| 59.6%; Score 2765; DB 3; Length 1171; 55.4%; Pred. No. 1.2e-162;                | ; Mismatches          |
| 59.68;  | ative 31              |
| Query Match 59.6%; Score 2765; DB Best Local Similarity 55.4%; Pred. No. 1.2e-3 | Matches 561; Conserva |

GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105 138 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAPGPPGPTGPAGPPGFPGAVGAKGEAGPO 197 78 GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGARGDAGPAGPKGEPGSPGENGAP 137 -GKDGEAGAQ 150 -----AGSPGFQGLPGPA 180 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA--- 57 18 GPMGPSGPRGLPGPPGAPGGPPGEPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP 77 -GVPGPPGAVGPA-106 GQAGVMGFPGPKGAAGEPGKAGER-GPPGPAGPAGERGEOGP----28 151 유 d ò ò δ 셤 ò 임

Primer, PCR, amplification; human, collagen, mammal, plant, prosthesis, cardiac valve, ligament, tendon, skin, gingival implant; perfumes; nerve regeneration, antibiotic; growth factor; cancer; inflammatory; gelatin; glue, food

Human recombinant collagen protein.

(first entry)

08-DEC-1998

AAW68485;

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"cleavage site for carboxypeptidase"

/note=

WO9827202-A1

35-JUN-1998.

437

97WO-FR002331. 96FR-00016224.

17-DEC-1997; 17-DEC-1996;

'note= "cleavage site for aminopeptidase"

"signal peptide" "mature protein"

988. note=

> Cleavage-site Cleavage-site

note=

Peptide Protein

Location/Qualifiers

Homo sapiens.

Synthetic

GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 393 GLTGSPGSPGPDGKTGPPGPAGDGRPGPPGPPGARGQAGVMGPPGPKGAAGBPGKAGER 378 334

QC ò

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678 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 737

GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618 738 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPOGIAGOR 797

562

The invention relates to the production of mammalian collagen in plants. 2 clones: alpha3 and alpha22, spanning the human collagen type I gene were isolated from a NG-63 osteosarcoma library. Clone alpha3 contained 83 bp of the 5' untranslated region and the first 1920 bp of coding sequence, whereas clone alpha22 contained sequence encoding amino acids 

in and New recombinant nucleic acid for expressing collagen or derivatives plants - useful as, e.g. bio-materials and in therapeutic, cosmetic Merot B; Garrone R, Comte J, ſĽ, Ruggiero plants - useful as, e.g. bi odontological compositions. Exposito J, WPI; 1998-362771/31. N-PSDB, AAV60814. (BIOC-) BIOCEM Gruber V, Bournat P;

Disclosure; Fig 7; 138pp; French.

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The 2 clones were used to generate a number of fragments which were used to construct composite sequences encoding variant collagen molecules. The fragments are: (A) containing nucleotides (nt) -4 to 479; (B) containing proteins are to expensive the sequence encoding the PRS (pathogenesis-related TAA upstream of the sequence encoding the PRS (pathogenesis-related CC TAA upstream of the sequence encoding the PRS (pathogenesis-related the protein of Dases 66-77 from the sequence encoding the CC TAA upstream of the pro-collagen amino propeptide domain; (C) the whole of the amino propeptide domain (nt 72-479); (D) all of the amino-telopeptide commin (nt 474-534) and the N-terminus of the Helicoidal region (nt 535-1920); (E) the DraIII-Bamil fragment (1709-2808) of alpha22, encoding as 56-1936 of the central helicoidal domain; (G) the C-terminus of the C-terminus of and as 1193-1454 in the C-propeptide domain; (G) the C-terminus of the C-terminus of an 1343-140 and also including the NDEL motified and and (G).

CC propeptide domain (as 1346-1464) plus stop codons, and (H) as G but the BR. This sequence represents a recombinant human collagen. The encoding an 1343-140 and also including the NDEL motified (F) and (G).

CC propeptide compresses or prometation in the C-terminus of the C-terminus gene is used for expression of mammalian collagen. The encombinant gene is used for expression of mammalian collagen. The plant cells. The transformed plants, their extracts and parts are useful as blomaterials (medical, odontological, cosmetic and parts are useful compositions (e.g. as prostheses for cardiac valves, ligaments or tendons; skin substitutes; gingival implants; microcapsules for nettines; guide trubes for netters are related provent factors anticance antical and parts are surgical trubes; for netters surgical through and also an antical and parts are surgical trubes. Secured and parts are surgical encoding and an analysism and an analysism and an antical and and an analysism and an antical and and an antical and an growth factors, anticancer agents or anti-inflammatories; surgical thread and components of ointments). They are suitable for treating any disorder related to collagen dysfunction and gelatin, produced from collagen, is used to produce glues, surgical prostheses and foods 888888888888888888888888888888888

Sequence 1464 AA;

238 105 298 150 299 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGPPGAVGAKGEAGPQ 358 180 418 478 273 538 333 GLTGSPGSPGPPGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 598 393 GEGGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP 718 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGBAGLP 474 GPPGEAGKPGEQGVPGDLGAP-----GEPGPT 213 .----TGLPGPP 423 359 GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGOPGAKGANGAPGIAGAPGPPGARGPS 58 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP 179 GPMGPSGPRGLPGPPGAPGGPOGFOGPPGBPGASGPMGPRGPPGPPGKNGDDGEAGKP GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ --- AGSPGFOGLPGPA GPOGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---Gaps , Score 2765, DB 2, Length 1464, Pred. No. 1.5e-162, 31; Mismatches 228; Indels 192; GEOGVPGDLGAPGPSGPAGE------PGP----PGP-Ouery Match Best Local Similarity 55.4%; Matches 561; Conservative 3: GPPGPAGPAGERGEQGP 239 106 151 181 419 214 479 274 539 334 599 394 124 g d ò a ò DP DP \$ g ò ò ò ઠે g ò d ò 9

.079 Ġ₽ĀĠĀŖĠPĀĠPŖĠPŖĠPŖĠEŖĠEŖĠEŖĠEŖĠŦĸĠĦŖĠŖĠĠŖĠŖŦĠŖŖŦĸĠŖŶ 1138 959 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1018 The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 839 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP 898 618 for GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 899 Ġ₽AĠKEGGKĠPŔĠĔŢĠ₽AĠŖPĠEVĠPPĠPPĠPAĠEKĠSPĠADĠPAĠAPĠŢPĠPQĠĮĀĠQŖ 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGODGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 719 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal. 516 ----AGVMGFPGPKGAAGBPGKAGBRGVPGPPGA------VGPAGKDGEAGAQGPP Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG -----GLTGSPGSPGFDGKTGPPGPAGQDGRPGPPGARGQ-Σ Costigan Human Protein P02452, SEQ ID NO 10491. A. standard; protein; 1464 Claim 1; Page; 1017pp; English. Befort K, 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-033347P. 14-AUG-2002; 2002WO-US025765. (first entry) (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG. Woolf C, D'urso D, WPI; 2003-268312/26. WO2003016475-A2. GENBANK, P02452 Homo sapiens 29-JAN-2004 27-FEB-2003 262 619 736 ADD45059 ADD45059; 772 RESULT 10 ADD45059 셤 셤 ò 셤 В  $\delta$ 임 ò 염 ò 8 8 g · 8

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claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a fit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates an enthod for identifying a compound useful in treating computed to a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more construction or pain and a sequence presented for preparing a medicament for treating computes its sequence presented is a human proceed or the compound that compute or spain (e.g. spainal segmental nerve injury (CUIN and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human proceed (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed specification, but was obtained an electronic form directly from WIPO at the wibo. Int. Vnh. Vnullished not, securing form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGASGPMGPRGPPGPPGRNGDDGEAGKP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGOPGAKGANGAPGIAGAPGFPGARGPS 418
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llarity 55.4%; Pred. No. 1.5e-162;
Conservative 31; Mismatches 228;
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ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
Matches 561; Conserv
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959 GWGLPGQRGERGFPGLPGBPGKQGPSGASGERGPPGPWGPPGLAGPPGESGREGAP 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAGARGPAGPQGPRGDKGETGEQGDRGIXGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 1138
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779 GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGFAGPPGADGQPGAKGEPGDAGAKGDA 838
                                                                                                              GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                   GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                         GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
                                                                                                                                                                                                                                                                                                                                                                                             GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                     ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGBAGAQGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           736 GKAGERGVPGPPGAVGPAGKDGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein P02452, SEQ ID NO 10487.
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pain; neuronal tissue; gene therapy; segmental nerve injury; chronic constriction injury; CCI; nerve injury; SNI; Chung. spared spinal

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765 WO2003016475-A2. Homo sapiens. 27-FEB-2003.

Costigan M; Befort K, (GEHO ) GEN HOSPITAL CORP. D'urso D, FARB ) BAYER AG. Woolf C,

2003-268312/26. GENBANK; P02452

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal. Claim 1; Page; 1017pp; English.

that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating or pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (Ct) and spared nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed frp.wipo.int/pub/published\_pct\_sequences. %XGGGGGGGGGGGGGGGGGGGGGGG

## Sequence 1464 AA;

59.6%; Score 2765; DB 7; Length 1464; 55.4%; Pred. No. 1.5e-162; ive 31; Mismatches 228; Indels 192; Gaps Matches 561; Conservative Similarity Query Match Local

179 GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGASGPMGPRGPPGPPGRNGDDGEAGKP 238 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---셤

105 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 58

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----AGSPGFQGLPGPA 180 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 358 359 GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS GPPGPAGPAGERGEQGP------299 151

GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPCAK GPPGEAGKPGEQGVPGDLGAP------GPSGPA----GESGPAT 214 181

GLPGPPGERGGPGSRGFPGADGVAGPRGPAGERGSPGPAGPRGSPGEAGRPGEAGLPGAK GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 539 GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 479 274

423 GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGEAGEQGPAGSPGFQGLPGPAGPPGEAGKP 334 599

GEQGVPGDLGAPGPSGPAGE------PGP-----PTGLPGPP GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP

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Db

GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE------AGRPGEAGLP GAK------GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ-------424 719 475

----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP 561

516

GVVGLPGQRGBRĞFPGLPGPSGEPGKQGPSGASGERGPPGPPGFPGERGAPPO1018 1019 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV 1078 1138 dpagkeggkgpkgerdpagkpgevgppgppgpgpgekgspgadgpagapgrpgpgglaggr 736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP-----AGPA 1079 GPAGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPA 839 GPPGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP GPAGP----AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAAGEP 1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPG 1190 GERGERGGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820 619 959 919 899 772 562 g g ð ò D. 8 셤 8 ò

Human Protein P02452, SEQ ID NO 10483. ADD45051 standard; protein; 1464 AA. (first entry) 29-JAN-2004 ADD45051; ADD4505 

Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

WO2003016475-A2. Homo sapiens

27-FEB-2003.

418

213 478 273

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-033347P. 14-AUG-2002; 2002WO-US025765

Costigan M; Befort K, (GEHO ) GEN HOSPITAL CORP. (PARB ) BAYER AG. Woolf C, D'urso D,

WPI; 2003-268312/26 GENBANK; P02452.

598 393 658

538 333 New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

718

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, edivivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially

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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the particlesticaes, an enthod for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymorlectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Rung), chronic constriction injury (CLI) and spared nerve injury (RUNJ) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                   GPMGPSGPRGLPGPPGAPGPQGPPGEPGEPGASGPMGPRGPPGPPGRNGDDGEAGKP 238
                                                                                                                                                                                                                                                                                                                                                              GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR 105
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                                                                                                                                                                                                                                                       59.6%; Score 2765; DB 7; Length 1464;
55.4%; Pred. No. 1.5e-162;
ive 31; Mismatches 228; Indels 192;
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Best Local Similarity
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399 GPAGKEGGKGPRGETGPAGRPGEVGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
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                                                                                                                                            GVVGLPGORGERGFPGLPGPSGEPGKOGPSGASGERGPPGPMGPPGLAGPPGESGREGAP
                                                                                                                                                                                                                      GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
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                                                                      619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; deer; rat; mouse; DACC; deer antler cartilage cell; cell stimulation; cell inhibition; cell growth; cell division; mesenchymal cell; chondrocyte; chondrogenesis; osteogenesis; growth; repair; regeneration; rescoration; extracellular matrix; cartilaginous matrix; cartilage; disc; connective tissue; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPGPPG 1190
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                                                                                                                                                                                                                                                                                                                                                                              ----AGAOGPPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide orthologous to DACC-11.
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                                                                                                                                                                                                                                                                                                                                                                       GKAGERGVPGPPGAVGPAGKDGE-
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growth and/or division by inserting into an animal cell, a compound which inhibits the translation of the polymelectide encoding the DACC. The method and the polypeptides are useful for stimulating mesenchymal cell growth and/or division or for stimulating chondrogenesis, cartilage, or connective tissue growth, repair, regeneration and/or restoration in an animal. The polymelectides, polypeptides, agonists and antagonists may be used in treatment modalities, specifically in gene therapy. The polypeptides can be used as bait proteins in a two- or three-hybrid assay to identify other proteins, which bind to or interact with the polypeptide and are involved in modulating cell growth and/or division. The sequences presented in ABG93923-ABG93948 are the proteins encoded by the DACC cDNA clones 

Sequence 1461 AA;

775 515 561 895 618 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA 675 474 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGOR 955 393 655 423 180 415 213 273 535 333 595 235 105 GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAP 295 GQAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA------GKDGEAGAQ 150 GPQGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT 475 gppgpagpagppgprignvgapgaxgakgagppgpgagrofpgaagrygppgppgpp GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKP GVPGPPGAVGPAGKDGBAGAQGPPGPAGPAGBRGBQGPAGSPGFQGLPGPAGPPGBAGKP 656 GEĞGVPGDLGAPGPSGARGERGFPGERGVOGPPGPAGPRGANGAPGNDGAKGDAGAPGAP GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLP GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP GAK------GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQ------GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPPGADGQPGAKGEPGDAGAKGDA ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPP GPAGP----AGERGEOGPAGSPGFPGGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEP GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGBPGASGPMGPRGPPGPPGKNGDDGEAGKP GONGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPO ---AGSPGFQGLPGPA GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS GLTGSPGSPGCKTGPPGPAGQDGRPGPPGPPGARGQAGWGFPGPKGAAGBPGKAGER 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA--------DGKTGPPGPAGQDGRPGPPGPR Length 1461; Indels GEQGVPGDLGAPGPSGPAGE------PGP-----Score 2761; DB 5; Pred. No. 2.6e-162; 1; Mismatches 229; GRPGEAGLP -- GAKGLTGSPGSPGP-GPPGPAGPAGERGEQGP-----31; GPPGEAGKPGEQGVPGDLGAP 59.5%; Conservative Similarity Matches 560; 424 562 716 516 836 596 475 236 296 356 416 214 476 274 536 334 394 9/1 28 181 901 151 Local Пр  $\delta$ d ò g ò 임 ò d ò 원  $\stackrel{\circ}{\sigma}$ g à ò g 엄 ò 셤 8 q ò à g  $\stackrel{>}{\circ}$ 

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the invention relates to polymucleotides encoding novel human proteins or their active domains. The polypeptides, polymucleotides and antibodies caused against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides can be used to identify compounds which bind to the polypeptides. Polymucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in generating the encompinant proteins, and in generating anti-sense DNA or RNA and in generating the encompinant proteins of the invention can be used to target drugs to antibodies/elicit an immune response, to determine quantitative protein levels as tissue markers, and to isolate receptors or ligands.

Tolypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, segenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting 1075 devdakdepadepoderdendendendentkonrorsdiodepedergergerscasden 1135 in gene 771 immunomodulatory, cytostatic, neuroprotective, vulnerary, nootropic, anticonvulsant, antiarthritic, cerebroprotective, antifungal, antiviral, antibacterial, antiallergic, dermatological, haemostatic, antiasthmatic, thrombolytic, immunogen, antibody, gene therapy; neurological disorder; parkinson's disease, inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPV GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP diseases, GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG 1187 Isolated polypeptides useful for treating anti-inflammatory diseas nervous system disorders, and for regenerating bone and cartilage. protein; Antianaemic; osteopathic; antiinflammatory; GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG -----AGAQGPPGP-English. AAU14136 standard; protein; 1464 AA GKAGERGVPGPPGAVGPAGKDGE-525-527; 894pp; 25-JAN-2001; 2001WO-US002623. 25-JAN-2000; 2000US-00491404. RT Drmanac entry) Human novel protein #7. 2001-451939/48. (first (HYSE-) HYSEQ INC. rang YT, Liu C, N-PSDB; AAS22441 Example 4; Page WO200155437-A2 Homo sapiens. 02-AUG-2001. 24-OCT-2001 1016 1076 AAU14136; 772 1136 926 919 736 RESULT 14
AAU14136
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the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fingal infection or from autoimmunity, cancer, allergy, asthma, graftversus-host diseases, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention
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                                                                                                                                                                                                                           Indels 192;
                                                                                                                                                                                            Length 1464;
                                                                                                                                                                                       Query Match
59.5%; Score 2761; DB 4; :
Best Local Similarity 55.3%; Pred. No. 2.6e-162;
Matches 560; Conservative 31; Mismatches 229;
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The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-6 hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibrinogen and production of proteins such as collagen, fibrinogen and proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of protein, which may be produced using the method of the invention
.019 GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPAGPV 1078
                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix protein; self aggregation; hydroxylated proline; trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibrinogen; fibronectin; post translational hydroxylation.
                                          --AGPA
                                                                          GPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGEQGPSGASGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxyproline results in native self aggregating proteins, useful on medical implants.
                                                                                                                                       1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRIGDAGPVGPPGPPGPPG 1190
                                                                                                                   820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of extracellular matrix proteins containing 4-trans-
                                                                                                             772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human collagen 1 (alphal) protein.
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Pred. No. 2.7e-162;
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                                    GKAGERGVPGPPGAVGPAGKDGE
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Best Local Similarity
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562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618
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                                                    181 GPPGEAGKPGEQGVPGDLGAP----GEPGPA----GEPGPA
                                 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
560; Conservative 31; Mismatches 229; Indels 192; Gaps
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Search completed: October 18, 2004, 13:37:32 Job time : 135.602 secs

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
version 5.1.6
- 2004 Compugen Ltd.
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US-09-585-887-9

US-08-9281-820-1

US-08-953-825-18

US-09-500-811-18

US-09-500-811-18

US-09-500-811-18

US-09-500-811-18

US-09-500-811-18

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Maximum Match 100%
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Match 1
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US-09-331-347C-21
US-09-331-347C-21
Sequence 21, Application US/09331347C
Patent No. 6617431
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics, S.A.
TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, N. TITLE OF INVENTION: Recombinant Collagens and Their Uses
TITLE OF INVENTION: Detailing Such and Their Uses
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT APPLICATION NUMBER: US/09/331,347C
CURRENT FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
Language 1.6.4
Language 2.6.4
Language 2.6
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110, Appl
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llarity 55.4%; Pred. No. 2.9e-171;
Conservative 31; Mismatches 228;
US-09-548-608-19
US-09-588-887-10
US-09-589-578-10
US-08-642-255-10
US-09-919-499-5
US-09-219-499-5
US-09-219-499-5
US-09-219-499-5
US-09-219-849-5
US-09-219-849-5
US-09-219-849-5
US-09-219-849-50
US-09-175-155-68
US-08-477-5038-103
US-08-477-5038-103
US-08-477-5038-103
US-08-642-255-101
US-08-642-255-103
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     ORGANISM: Homo sapiens
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   Query Match
Best Local Simil
Matches 561; C
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                                                             GPAGP---AGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                                               676 GLEGAKGLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQAGVMGPPGPKGAAGEP
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                                                                                                       896 GPAGKEGGKGPRGETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGAPGTPGPQGIAGQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for collagen degradation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
CLASSIFICATION 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08931820
Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Assay for coll
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
MEDIUM TYPE: Floppy disk
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Collagen type I
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1i
MOLECULE TYPE:
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TISSUE TYPE:
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Best Local &
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                                                             APPLICANT: Olsen, David R
APPLICANT: Chang, Robert
APPLICANT: Chang, Robert
APPLICANT: McMullin, Huber
APPLICANT: McMullin, Huber
APPLICANT: McMullin, Huber
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Hitzeman, Ronald A.
APPLICANT: Chisholm, George
TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND
TITLE OF INVENTION: CELLS
FILE REFERENCE: 225002030400
CURRENT APPLICATION NUMBER: US/09/289,578
CURRENT FILING DATE: 1999-04-10
PRIOR PLILING DATE: 1999-04-10
PRIOR PLILING DATE: 1999-05-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN UNCE: 2.0
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        Sequence 9, Application US/09289578 Patent No. 6428978
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Matches 559; Conșervative
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US-09-289-578-9
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
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INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
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                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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New York
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Matches 542; Conserv
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                COUNTRY:
                                                                                                            SOFTWARE
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                                                             -GPAGEPGPTGLPGPPGERGGPGSRGFPGADGVA 237
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                    GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 401
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US-08-963-825-18
Sequence 18, Application US/08963825
Sequence 18, Application US/08963825
Fatent No. 6110689
GENERAL INFORMATION:
APPLICANT: Ovisit, Per
APPLICANT: Original Amethod for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carr
TITLE OF INVENTION: Method and Use of the Method to Diagnose the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barby RC
STREET: 805 Third Avenue
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                                                                                                 PatentIn Release #1.0, Version #1.25
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FILING DATE:

CLASSIPICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/187,319

FILING DATE: 21-JAM-1994

ATTORNEY, AGENT INFORMATION:

NAME: GOGOTIS, Adda C

REGISTRATION NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 4305/0870

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4305/08701
                                                                                                                             DATA:
r: US/08/963,825
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                       Indels 132;
                                                                                                                                                                                               Length 1341;
                                                                                                                                                                                               Query Match 58.3%; Score 2704; DB 3; Best Local, Similarity 57.3%; Pred. No. 2.3e-167; Matches 542; Conservative 28; Mismatches 244;
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                                                                                                              IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1
US-09-500-811-18
                                                                                                 ORGANISM: Homo sapiens
                                                         protein
                   TYPE: amino acid TOPOLOGY: linear
                                                       MOLECULE TYPE: ORIGINAL SOURCE:
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Sequence 18, Application US/09500811

Patent No. 632314

GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCE ADDRESS:
ADDRESSES: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STREET: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 GPAGPOGPRGDKGETGEQGDRGIKGHRGFSGLOGPPGPPGSPGSQGPSGASGPAGPRGPP 1020
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516
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                                                                                               GPSGPAGPTGARGAPGDRGEPGPPGPAGPPGADGQPGAKGEPGDAGAKGDAGPPGPA
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                                                           -----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ANDER ACTORNEY ACRONICATION:
NUMBER: GOODTIE AND ACTORNEY ACRONICATION:
NUMBER: GOODTIE AND ACTORNEY ACRONICATION:
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REGISTRATION NUMBER: 29,714
REPRENCE/DOCKET NUMBER: 4305.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEKAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPGPPGAVGPAGKDGE
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US-09-500-811-18
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Carrying Out to the Presence of
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GERGEQGPAGSPGFPGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPP 219
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                                                                                                                                                              GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP 339
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                                      GNSGE-----PGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLPGPP
                                                                               GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP
                                                                                                         361 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLIGSP
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APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A method and Use of the Method to Diagnose the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESSED: ADDRESS:
ADDRESSE: Buthy & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 GPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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US-09-548-608-18
; Sequence 18, Application US/09548608
; Patent No. 6355442
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                      Sequence 18, Application US/09570573

Patent No. 6342361

GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                       ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPPGE---PGPTGLPGPPGERGGPGSRGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: GOGOTIS, Adda C
REGISTRATION UNUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305,
TELECOMMUNICATION INFORMATION:
TELERAN: 212-527-7700
TELERAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue CITY: New York CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (1)
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Best Local Similarity
Matches 542; Conserv
                       GPAGSP-
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APPLICANT: VAN HEBENE, GEORGE V.
APPLICANT: VAN HEBENE, JAN B.
APPLICANT: PAN HEBENE, JAN B.
APPLICANT: DE WOLE, FREDENIK A.
APPLICANT: DE WOLE, FREDENIK A.
APPLICANT: WOOBROEK, ANDREAS
APPLICANT: WOOBROEK, ANDREAS
APPLICANT: WOOBROEK, ANDREAS
APPLICANT: WOOBROEK, ANDREAS
APPLICANT: WAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE
TITLE OF INVENTION: SULTABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION OF SILVER HALIDE
GURRENT APPLICATION NUMBER: US/09/219,849
CURRENT APPLICATION NUMBER: US/09/219,849
SOFTWARE: PAUGHLIN VOY: 2.1
SEQ ID NOS: 50
SETTAMES PAUGHLIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       961 GPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPAGPRGPP 1020
                                                                                                                                                                                   781 GGKGPRGETGPAGRPGEVGPPGPPGPPGBKGSPGADGPAGAPGTPGPQGIAGQRGVVGLP
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                                                                                            721 GPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPAGKE
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                                                                                                                                         --AGERGEQGPAGSPGFPGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLP
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
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Best Local Similarity 56.6%; Pred. No. 4.4e-155;
Matches 498; Conservative 35; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 49, Application US/09219849; Patent No. 6150081; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNSGE-----PGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPTGLPGPP 360
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GGOGNIS, Add C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
RELEPAX: 212-753-6237
TELEPAX: 212-753-6237
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.3%; Score 2704; DB 3;
Best Local Similarity 57.3%; Pred. No. 2.3e-167;
Matches 542; Conservative 28; Mismatches 244;
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (1)
US-09-548-608-18
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GY: linear
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PRIOR FILING DATE: 1990-03-02
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR FILING DATE: 1990-07-14
PRIOR FILING DATE: 1989-07-14
PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
PRIOR FILING DATE: 1990-10-31
PRIOR FILING DATE: 1990-10-31
SOFTWARE: PATENTING DATE: 1990-10-10
SOFTWARE: PATENTING DATE: 1990-10-10
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                                                                                                                                                                     ; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-468-996-10
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       GNSGEPGAPGNKGDTGAKGEPGATGVQGPPGPAGEEGKRGARGEPGPSGLPGPPGERGGP
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GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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-KGLT
                                                        -----AGODGRPGPPGPPGARGOAGVMGFPGPKGAAGEP
                                                                                   GAPGAPGPPGSPGPAGPTGKQGDRGEAGAQGPMGPSGPAGARGIQGPQGPRGDKGEAGEP
                                                                                                                GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA
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ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                         ATREET: 4 EMBARCAGETO CENTER, SUITE 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.4%; Score 2478; DB 1;
53.8%; Pred. No. 7.5e-153;
ive 33; Mismatches 281;
GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA
                                                                                                                                                                                                       GPPGPRGRSGBTGPAGPPGNPGPPGPPG 1012
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NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 62, Application US/08642255
Patent No. 577349
GENERAL INFORMATION:
APPLICANT: CARPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weigh
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                            GPPGEAGKPGEQGVPGDLGAPGPSGPAG
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TELEFAX: (415) 494-8771
TELEEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
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                                                          GSPGSPGPDGKTGPPGP
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Best Local Similarity 53.8
Matches 506; Conservative
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MOLECULE TYPE: protein
US-08-642-255-62
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US-08-642-255-62
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                                                      160 GAPGPAGPPGSRGDPGPPGAPGPPGSRGDPGPPGAPGPAGPPGSRGDPGPPGAPGPA 219
                                                                                                                                        169 GSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGP---AGEPGPTGLPGPPGERGGP 225
                                                                                                                                                                                                      220 GPPGSRGDPGPPGAPGPAGPPGSRGDPGAPGPAGPPGSRGDPGAHGPAGPKGAH 279
                                                                                                                                                                                                                                                                                    226 GSRGFPGADGVAGPK---GPAGERGSPGPAGPKGS---PGEAGRPGEAGLPGAKGLTGSP 279
                                                                                                                                                                                                                                                                                                                                                          280 gpagpkgangpagpkgangpagpkgapgpagpgskgDpgspgapgapgpagppgskgDpgpp 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 GSPGS---PGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 GVPGPPGAVGPAGKDGEAGAQGP---PGPAGPAGERGE-----QGPAGSPGFQGLPGPA 588
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GAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGP---PGPAGPAGERGE-
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TITLE OF INVENTION: Assay for collagen degradation
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EP
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Qvist. Per
APPLICANT: Qvist. Per
APPLICANT: Qvist. Per
APPLICANT: Qvist. Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            736 GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGBAGERGEQGPAGSPGFQGLPGPA
                                               824 GOQGAPGASGDRGPPGPVGPPGLTGPAGEPGREGSPGADGPPGRDGAAGVKGDRGETGAV
                                                                                             ----AGODGRPGPPGARGQAGVMGFPGPKGAAGEP
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           GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA
                                                                                                                                                                                                                                                                                             1004 GPPGPRGRSGETGPAGPPGNPGPPGPPG 1031
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29,714
205/08701
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFRENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1418 amino acids
                                                                                             GSPGSPGPDGKTGPPGP
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 503; Conserva
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US-08-963-825-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGSPGFP 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GODGRPGPPGPPGARGOAGVMGFP-----GPKGAAGEPGKAGERGVPGPPGAVGPA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 GASGNPGTDGIPGÁKGSAGAPGIÁGAPGFPGPRGPPDPQGATGPLGPKGOTGKPGIAGFK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 GPKGAPGERGPSGLAGPKGANGDPGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 524 GERGSPGAQGLQGPRGLPGTPGTDGPKGASGPAGPPGAQGPPGLQGMPGERGAAGIAGPK 583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP-----GKA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 GETGPPGTSGIAGPPGADGQPGAKGEQGBAGQKGDAGAPGAPGAPGAPGPQGPTGVTGPK 703
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                                                                                                                                                                                                                                                                                                                                                                                                                 168;
                                                                                                                                                                                                                                                                                                                                                                      53.4%; Score 2476; DB 3; Length 1060; 50.9%; Pred. No. 1e-152; ive 45; Mismatches 272; Indels 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GEAGL PGAKGLTGSP---GSPGP
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GD---LGAPGPSGPAGEPGPTGLP---
                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type II
                                                                                          <u>۳</u>
                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                              single
                                                                                                                               LENGTH: 1060 amino
TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 503; Conserv
                                                                                                                                                                                                                                                                                                                             US-08-931-820-3
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| APPLICANT: Poole, Anthony R. APPLICANT: Hollander, Anthony P. APPLICANT: Billinghurst, R. C. TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Folly & Lardner STREET: 3000 K Street, N.W., Suite 500 STREET: 0.C. CITY: Washington STREET: 0.C. COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: PROBABLE FORM: | COMPUTER: IBM PC Compatible COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/010,999 FILING DATE: 22-JAN-1998 CLASSIFICATION: 4335 | PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 08/448,501  FILING DATE: 17UL-1995  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 07/984,123  FILING DATE: 04-DEC-1992  ATTORNEY/AGENT INPORMATION:  NAME: Bent, Stephen A. | REGISTRATION NUMBER: 29,768<br>  REFERENCE/DOCKET NUMBER: 032931/0212<br>  TELECOMMUNICATION INFORMATION:<br>  TELEPHONE: (202) 672.5300 | " "Fo        | amino acid DNESS: Y: linear   | ; CRIGINAL SOURCE: ; ORGANISM: Human Type II Collagen<br>US-09-010-999-1 | Query Match 53.4%; Score 2476; DB 3; Length 1418; Best Local Similarity 50.9%; Pred. No. 1.3e-152; Matches 503; Conservative 45; Mismatches 272; Indels 168; Gaps 17; | OY 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGEAGRP 60 | Qy 61 GEAGLPGAKGLTGSPGSPGP DGKTGPPGPA 90                    | OY 91 GQDGRPGPPGARQQACVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 141           | QY       142GKDGBAGAQGPPGPAGPRGBQGPAGSPGFPGGLPGPAGPPGBAGKPGEQGUP 195         DD       336 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 395 | Qy         196 GDLGAPGEPGEPGEPGTGLPGPPGERGGPGSRGFPGADGVA 237           Db         396 GEQGPKGEPGPAGPEGKRGARGEPGGVGPTGPPGERGAPGNRGFPGQDGLA 455           Qy         238 GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPPAGQD 297           IIII |
|--|--|---|--|--------------|---|--|---|---|---|--|--|--|
|  | Oy 196 GDLGAPGPSGPAGEPGPTGLPGPPGERGAPGSRGFPGADGVA 237  | Oy 298 GRPGPPGPRGQAGVMGFPGPKGAAGERGVPGPPGAVGPAGKDGEAGAGGPP 357  | Qy 414PGPTGLPGPPGERGGPGSRGPPGADGVAGPKGPA 447   | QY 448 GERGS | OY 484 GSPGPDGKTGPPGPAGODGRPGPPGAKGQAGWGPPGPKGAAGEPGKA 534  DD 756 GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815 | QY 535 GERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQ 582              | OY 583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGBRGGPGSKGFPGAD 642   | OY 643 GVAGPKGPAGERGSPGPAGPKGSPGEAGLPGAKGLT 684             | QY 685 GSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGWMGFPGPKGAAGBP 735 | QY 736 GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGBRGEQGPAGSPGFQGLPGPA 792 | Cy         793 GPPGEAGKPGEDGGVPGDLGAPGPSGPAG 820           DD         1116 GPPGPRGRSGETGPAGPPGNPGPPGPPG  | SULT 14<br>-09-010-999-<br>Sequence 1,<br>Patent No.   |

238 GPKGPAGERGSPGPAGPKGSPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 297

RESULT 14
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:

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216 GVKGHRGYPGLDGAKGEAGAPGVKCESGSPGENGSPGPMGPRGLPGERGRTGPAGAR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GPPGERGGPGSRGFPGADGVA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.4%; Score 2476; DB 3; Length 1.
50.9%; Pred. No. 1.3e-152;
ive 45; Mismatches 272; Indels
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                                                               08/187,319
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IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                    NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELERAK: 212-527-7700
TELERAK: 212-537-770
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.9
Matches 503; Conservative
  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                          amino acid
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                                                               GRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEKGLPGAPGLRGLPGKDGETGAEGPP 575
                                                                                                                                                GPAGPAGERGEQGAPGPSGFQGLPGPPGBPGBGGKPGDQGVPGBAGAPGLVGPRGERGFP 635
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                                                                                                                       GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
                                                                                                                                                                                                       ---GPPGERGGPGSRGFPGADGVAGPKGPA 447
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                                                                                                                                                                                                                                                                                    -----PGPAGPKGSPGEAGRPGEAGLPGAKGLTGSP 483
                                                                                                                                                                                                                                                                                                                                                                                                     GETGPPGTSGIAGPPGADGQPGAKGEQGEAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 815
                                                                                                                                                                                                                                                                                                                                                                                                                                             GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ 582
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GPKGAPGERGPSGLAGPKGANGDPGRPGEPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 515
                                                                                                                                                                                                                                                                                                                        696 GDRGDVGEKGPEGAPGKDGGRGLIGPIGPPGPAGANGEKGEVGPPGPAGSAGARGAPGER 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLOGPAGPPGEKGEPGDDGPSGAEGPPGPQGLAGQRGIVGLPGQRGERGFPGLPGPSGEP
                                                                                                                                                                                                                                                                                                                                                                GSPGPDGKTGPPGPAGQDGRPGPPGPRGQAGVMGFPGPKGAAGEP-----GKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPGSPGPDGKTGPPGP-----AGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Qvist, Per
ATILE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carr
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 2
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1116 GPPGPRGRSGETGPAGPPGNPGPPGPPG 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGEAGKPGEOGVPGDLGAPGPSGPAG 820
                                                                                                                                                                                                     ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09500811
Patent No. 6323314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-500-811-20
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996 GAPGAPGPPGSPQPAGPTGKQGDRGEAGAGAMGPSGPAGARGIQGPQGPRGDKGEAGEP 1055
                                                                                                                                                                                      1056 GERGLKGHRGFTGLQGLPGPPGPSGDQASGPAGPSGPRGPPGPSGRDGANGIPGPI 1115
                                          685 GSPGSPGPDGKTGPPGP-----AGODGRPGPPGPPGARGOAGVMGFPGPKGAAGEP 735
                                                                                                                                                                          736 GK---AGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPA 792
                                                                                      643 GVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGA------KGLT 684
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October 18, 2004, 13:42:06; Search time 105.622 Seconds (without alignments) 2513.149 Million cell updates/sec
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4640
I GPPGEPGPTGLPGEPGERGG........GEQGVPGDLGAPGPSGPAGG 821
                                                                                                                                                                                                                                                                                                                                                                        1360919
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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                                                   OM protein - protein search, using sw model
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Perfect score:
Sequence:
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                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                | 80              | Sequence 8, Appli | Sequence 20, Appl | Sequence 11, Appl | Seguence 8, Appli | 10,              | Seguence 21, Appl | Sequence 1, Appli | Sequence 1, Appli | Sequence 150, App | 25, #            | Sequence 243, App | Sequence 16, Appl | Sequence 261, App |
|----------------------------|-----------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|
| QΙ                         | US-10-402-089-8 | US-10-402-072A-8  | US-10-104-889-20  | US-10-104-889-11  | US-10-104-889-8   | US-10-104-889-10 | US-10-216-705-21  | US-10-357-851-1   | US-10-358-024-1   | US-10-788-792-150 | US-10-468-091-25 | US-10-291-265-243 | US-10-104-889-16  | US-09-918-715-261 |
| DB                         | 15              | 12                | 12                | 15                | 15                | 15               | 14                | 16                | 16                | 17                | 16               | 14                | 15                | 10                |
| %<br>Query<br>Match Length | 1449            | 1449              | 1057              | 1107              | 1171              | 1388             | 1464              | 1464              | 1464              | 1464              | 1461             | 1464              | 1057              | 1464              |
|                            |                 | 59.6              | 59.6              | 59.6              | 59.6              | 59.6             | 59.6              | 59.6              | 59.6              | 59.6              | 59.5             | 59.5              | 59.5              | 59.4              |
| Score                      | 65.5            | 2765.5            | 2765              | 2765              | 2765              | 2765             | 2765              | 2765              | 2765              | 2765              | 2761             | 2761              | 2759              | 2755              |
| Result<br>No.              | -               | 7                 | m                 | 4                 | ហ                 | φ                | 7                 | ω                 | σ                 | 10                | 11               | 12                | 13                | 14                |

| Sequence 159, App | edneuce  | 5            | ence 65      | 5       | equence 79   | equence 2,  | quence 2,    | w               | equence 26 |            | 4      | equence 1(    | equence 1, | equence 2(   |        | equence 48 | ednence e'      | equence 12     | equence 12 | equence 4,   | vo | equence 4, | equence 6, | equence 23    |        | equence 33 | Sequence 72, Appl | equence 3 | equence 3    | Sequence 103, App |
|-------------------|----------|--------------|--------------|---------|--------------|-------------|--------------|-----------------|------------|------------|--------|---------------|------------|--------------|--------|------------|-----------------|----------------|------------|--------------|----|------------|------------|---------------|--------|------------|-------------------|-----------|--------------|-------------------|
| -10-0             | 0-171-31 | -10-149-352- | -10-177-293- | 1-822-2 | -10-734-564- | -10-402-089 | -10-402-072A | US-10-104-889-6 | 8-091-2    | -10-058-12 | 31 - 4 | -10-639-286-1 | -10-194-4  | -10-058-124- | -10-46 | -10-194-44 | US-10-468-091-6 | -10-402-089-12 | -07        | -10-402-089- |    | -072       | 2-072A-    | -09-918-715-2 | -293-6 | -10-301-   | 57-021-7          | -10-357-8 | -10-358-024- | US-10-734-564-103 |
| 14                | 14       | 14           | 14           | 14      | 16           | 15          | 15           | 15              | 16         | 14         | 14     | 16            | 14         | 14           | 16     | 14         | 10              | 52             | 13         | 12           | 15 | 15         | 15         | 10            | 14     | 14         | 14                | 16        | 16           | 16                |
| 1464              | 46       | 4            | vo           | 4       | 46           | 46          | 46           | 1169            | 45         | 4          | 2      | н             | 10         | ч            | 41     | 9          | 48              | 46             | 1466       | 46           | 9  | 46         | 46         | 46            | 46     | 46         | 9                 | 46        | 46           | 46                |
| 59.4              | 59.4     | 59.4         | ٠.<br>م      | 59.4    | 59.4         | 6           | 6            | 59.3            | 8          | ω.         | 4,     | ω.            | ά.         | ω,           | 53.4   | ۳.         | ω.              | ä              | 51.8       | Ξ.           | ä  | -          | ä          | ä             | ä      | ä          | 51.1              | ä         | 51.1         | 51.1              |
| 2755              | ın       | 75           | 75           | 75      | 75           | 752.        | ς.           | 75              | N.         | 70         | 51     | 48            | 47         | 47           | 47     | 46         | 46              | 40             | 40         | 379.         | 6  | 379.       | 379.       | 37            | 37     | 37         | 37                | 37        | 37           | 37                |
| 15                | 16       | 17           | 18           | 19      | 20           | 21          | 22           | 23              | 24         | 25         | 26     | 27            | 28         | 29           | 30     | 31         | 32              | 33             | 34         | 35           | 36 | 37         | 38         | 39            | . 40   | 41         | 42                | 43        | 44           | 45                |

## ALIGNMENTS

| RESULT 1                                     |   |
|--|---|
| Sequence 8, Publication                      | -10'402'089'0<br>Sequence Application US/10402089<br>Publication No. US2004000563A1               |
| GENERAL INFORMATION:                         | DENATION:   |
| APPLICANT:                                   | Ŋ   |
| APPLICANT:                                   | Polarek, James W.   |
| APPLICANT: Seeley,<br>TITLE OF INVENTION:    | Seeley, Todd w.<br>VVENTION: PORCINE COLLAGENS AND GELATINS                                       |
| FILE REFERENCE:                              | ENCE: FP0402.3 CON  |
| CURRENT APE                                  | CURRENT APPLICATION NUMBER: US/10/402,089   |
| PRIOR APPLI                                  |   |
| PRIOR FILIN                                  | FILING DATE: 2000-11-10   |
|  | SEQ ID NOS: 72  |
| '  | PatentIn version 3.2  |
| SEQ ID NO 8                                  | (**   |
|  | ער בין איני איני איני איני איני איני איני אי  |
| ) ORGANISM: S<br>US-10-402-089-8             | Sus scrofa<br>-8  |
| Query Match                                  | 59.6%; Score 2765   |
| Best Local Similarity<br>Matches 559; Conser | Similarity 56.7%; Pred. No. 4.5e-131;<br>9; Conservative 32; Mismatches 226; Indels 169; Gaps 21; |
| 0y 1   | GPPGEPGPTGLPGPPGBRGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48   |
| Db 193                                       | GPPGAPGPQGPPGEPGEPGASGPMGPRGPPGFWGDDGEAGKPGRPGERGPPGPQ 252  |
| Qy 49  | GPKGSPGEAGRPGBAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQD 93  |
| Db 253                                       | GARGLPGTAGLPGMKGHRGPSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGER 312                                  |
| Qy 94  | GRPGPPGPPGARGOAGVMGFPGPKGAAGEPGKAGERGVFGPPGAVGPAGKDGEA 147  |
|  |   |

| Db 33                        | 313 GRPGPPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQGARGSEGPQGVR 372        | PRIOR FIL   |
|------------------------------|---|---|
| 0y 14                        | 148 GAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEO 192                       | NUMBER OF SE(   |
|                              |   | ; SEQ ID NO 8<br>; LENGTH: 1449                               |
| Qy 193                       | 3 GVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGP 225                                     | ; TYPE: PRT<br>; ORGANISM: Sus scrofa                         |
| Db 43                        | 433 GNSGEPGAPGSKGDTGAKGEPGPTGVQGPPGPAGEEGKRCARGEPGPAGLPGPPGERGGP 492        | US-10-402-0/2A-8  |
| Oy 22                        | GSRGFPQADGVAGPKGPAGERGSPGPAGPKGSPCEAGRPGEAGLPGAKCLTGSPGSPGPD                | Query Macon<br>Best Local Similarity<br>Matches 559; Conserva |
|                              | GSKGF PGADGVAGPKGFAGEKGS PGFAGPKGS PGEAGKPGEAGLPGAKGLTGS PGS PGPD           | Oy 1 GPPGEPGPTGI  |
| UY 286<br>Db 553             | b GRIGEPERFAGUOSERGEPEGERGAROOGGWGEPERKAAGEBEGKAGERGVEGPEGAVGPA 345         | <br> Db   |
|                              | GKDGRAGAOGPBGGBAGGBAGGBGGGBGGGBGGGBGGBGGBGGAGKBGBCGVBGDLGAP                 | Qy 49 GPKGSPGBAGR   |
|                              | GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQCLPGPPGFAGFPGEAGFPGEAGPGGAP                | 253   |
| Qy 406                       | GPSGPAGETGLPGPPTGLPGPPGE  | Oy 94 GRPGPPGPPGP   |
| Db 673                       | 3 GPSGARGERGFPGERGVQGPPGPRGARGANGAPGNDGAKGDAGAPGAPGSQGAPGLQGMP 732          | 010   |
| Qy 436                       |   | QY 149 GAÇGEFGERGE<br>             <br>Db 373 GRPGPPGBA       |
| Db 733                       | 3 GERGAAGIPGPKGDRGDAPKGADGAPGKDGVRGLIGPIGPPGPAGAPGDKGETGPEGPA 792           | 193   |
| Qy 487                       |   | 433   |
| 793                          | 3 GPTGARGARGDRGPRGPAGFAGPPGADGQPGAKGGPTGPPGPIGSVGAPGPKGARGS 852             | ה ער<br>די כי   |
| Qy 540                       | 0 PGPPGAVGPAGKDGBAGADGPPGPAGBAGBRGEDGPAGSPGFQGLPGP 587                      | 977   |
| Db 853                       |   | 493   |
| Qy 588                       | 8 AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGP 647          | 286   |
| Db 913                       | 3 PGPAGEKGSPGADGPAGAPGTPGPQGIAGQRGVVGLPGQRGERGFPGLPGPSGEPGKQGP 972          | 553   |
| Qy 648                       | KGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDG                             | 346   |
| Db 973                       |   | 613   |
| Qy 702                       | 2 AGODGRPGPPGARGOAGVMGPPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE 758                | Qy 406 GPSGPAGE   |
| н                            | PGAPGAPGPAGPAGKSGDRGETGPAGPAGPVGPVGPRGPAGPQGPRGDRGETGEGGD                   | Db 673 GPSGARGERGF  |
| Qy 759                       |   | Oy 436 GADGVAGPKGP  |
| Н                            | RGIKGHRGFSGLQGPPGPPGSPGEQGPSGASGPRGPPGSAGAPGKDGLNGLPGPIGP                   | Db 733 GERGAÁGLPGP  |
| Qy 795                       |   | 487   |
| 1150                         |   | 793   |
|                              |   | Oy 540 PGPPGA   |
| RESULT 2<br>US-10-402-07     | 2.8-8   | Db 853 AGPPGATGFPG  |
| ; Sequence E<br>; Publicatio | ; Sequence 8, Application US/10402072A<br>; Publication No. US20040018592A1 | Oy 588 AGPPGEAGKPG  |
| GENERAL IN APPLICANT         | FORMATION:<br>: Bell, Marcum P.   | Db 913 PGPAGEKGSPC  |
| , APPLICANT<br>, APPLICANT   | : Neff, Thomas B.<br>: Polarek, James W.                                    | Oy 648 KGPAGERGSPG  |
| ; APPLICANT                  | Seeley, Todd W.<br>INVENTION: BOVINE COLLAGENS AND GELATINS                 | Db 973 SGPSGERGPPG  |
| ; FILE REFE                  | 72  | Oy 702 AGQDGRPGPPG  |
| ; CURRENT F                  | CURRENT FILING DATE: 2003-03-26<br>PRIOR APPLICATION NUMBER: US 09/709,700  | Db 1030 PĠAPĠAPĠAPĠ   |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPAGPKGSPGEAGRPGEAGLPGAKGLTGSP---GSPGPD---GKTGPPGP 701
                                                                                                                                                                                                                                                                                                                                                                                                                  SLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARGQ---AGVMGFPGPKGAAGE---PGKAGERGVPGPPGAVGPAGKDGEA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPAGERGEOGP-----AGSPGFOGLPGPAGPPGEAGKPGEO 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GEPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGPD 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODGRPGPPGPPGARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPGPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAKGLTGSPGSP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JPAGQDGRPGP---PGPPGARGQAGVMGF----PGPKGAAGEPGKAGERGV 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGP 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dandpadapdrpdpodradordvolpdordpidepopposesporodp 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPGARGOAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGE--- 758
                                                                                                                                                                                                                                                                                   3LPGPPGERGGPGS-----RGFPGA-----DGVAGPAGERGSPGPA 48
                                                                                                                                                                                                                                                                                                                                                                      JRP------GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VGPAGKDGEAGAQGPPGPAGPAGE---RGEQGPAGSPGFQGLPGP
                                                                                                                                                                                             59.6%; Score 2765.5; DB 15; Length 1449; 56.7%; Pred. No. 4.5e-131; Attive 32; Mismatches 226; Indels 169; Gaps
000-11-10
: 72
                                           ersion 3.2
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| Db 199 GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 257 Qy 181 GPPGEAGKPGEQGVPGDLGAP | 258 GPQGPGPFGPFGRGSEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEFGPT 214 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK | DD 318 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGFKGSPGFAGFKGSFGEAGKPGEAGLFGAK 377 QY 274 GLTGSPGSPGSPGPDGXTGPPGPAGQDGRPGPPGARGQAGVMGPPGPPGAGEPGKAGER 333 DD 378 GLTGSPGSPGPDGXTGPPGPAGQDGRPGPPGARGQAGVMGPPGPKGAAGEPGKAGER 437 | OY 334 GVPGPPGANGFAGKDGBAGGPPGPAGBRGEDGBAGSPGFQGLPGPAGFPGEAGKP 393 | Qy         394 GEOGVPGDLGAPGRSGPAGEPGPTGLPGPP 423  | Qy 424 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRFPGEAGLP 474 | OY 475 GAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPRGQ                   | 516  | OY S62 GPAGPAGERGEQGPAGSPGFQGLPGPAGPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618  | OY 619 GPTGLPGPPGERGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEA 675  | Oy 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGDDGRPGPPGARGOAGWGPPGPKGAAGEP 735   1   1   1   1   1   1   1   1   1 | Qy         736 GKAGERGVPGPPGAVGPAGKDGBAGGPG 771 | Oy 772 GERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820<br>  | RESULT 4 US-10-104-889-11 ; Sequence 11, Application US/10104889 ; Publication No. US20040086961A1 | ; GENERAL INFORMATION:<br>; APPLICANT: GRUSKIN, ELLIOT A.<br>; EUBCHTER, DOUGLAS<br>; DEDOVAL TANF | DENCYAM, GUANG<br>SHANG, GUANGHUI<br>PAOLELLA, DAVID<br>TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES | NOMBER OF SEQUENCES: 50 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: DILWORTH & BARRESE ; STREET: 333 EARLE OVINGTON BOULEVARD | STATE: NY COUNTRY: U.S.A.                 |
|--|--|--|--|--|---|---|--|--|--|---|---|---|--|--|--|--|---|
|  |  |  |  |  |   |   |  |  |  |   |   |   |  |  |  |  |   |
| Qy 759AGAQGPPGPAGPAGERGEGGPAGSPGFQGLPGPAGP 794   | Qy 795 PGEAGKPGEQGVPGDLGAPGFSGPAG 820<br>  | RESULT 3 US-10-104-889-20 ; Sequence 20, Application US/10104889 ; Publication No. US20040086961A1 . CENERAL INFORMATION   | APPLICANT: GRUSKIN, BLLIOT A. BUECHTER, DOUGLAS BROKAW, JANE       | JEANG, GUANGHOI  TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES  NUMBER OF SEQUENCES: 50 |   | STATE: NY COUNTRY: U.S.A. ; ZIP. 11553 ; COMPITTE PERDAM: POPM. | MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 | NT APPLICATION DATA: APPLICATION NUBBR: US/10/104,889 FILING DATE: 22-Mar-2002 CLASSIFICATION: <unknown></unknown> | PRIOR APPLICATION NUMBER: US/09/169,768  * APPLICATION NUMBER: US/09/169,768  * ATTORNEY/AGENT INFORMATION:  * ATTORNEY/AGENT INFORMATION: | TELECONAUTOLATION   JEFREE   S  | ა<br>ეკე<br>ექ                                  | ; STRANDEDNESS: single ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-10-104-889-20 | . 80<br>Q1   | QY 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPRGERGSPGPAGPKGSPGEA 57                                  | OY 58 GRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGDGRPGPPGAR 105   | OY 106 GQAGVMGFPGPKGAAGEPCKAGERGVPGPPGAVGPAGKDGBAGAQ 150   | Qy 151 GPPGPAGPAGERGEQGPAGSPGFQGLPGPA 180 |

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562 GPAGP---AGERGEQGPAGSPGFQGLPGPAGFPGEAGKPGEQGVPGDLGAPGPSGPAGEP
                                                                                                                                                                                                                                                                                                                                                              678 GPPGPAGPAGPPGPIGNVGAPGAKGARGSAGPPGATGFPGAAGRVGPPGPSGNAGPPGPP
                                                                                                                                                                                                                                           619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEA
                                                                                                                                                                                                                                                                                     798 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP
                                                                                                                                                                                                                                                                                                                                  GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                      ---AGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           918 GPÁGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLÓGPPGPPGSPGEQGPSGASGPA
                                                                 ----VGPAGKDGEAGAOGPP
                                                                                                                                                                                             738 gpagkeggekgpræfræpagrpderoppeppepagræspgangapagregregragor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      978 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGFVGPPGPPGPPG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            772 GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10104889

Publication No. US20040086961A1

GENERAL INFORMATION:
GRUSKIN, ELLIOT A.
BROKAW, JANE
ZHANG, GUANGLAS

ROKAW, GUANGLUI

PROKEN, DAVID

TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: SO

CORRESPONDENCE ADDRESSE:
STREET: 333 EARLE OVINGTON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                      736 GKAGERGVPGPPGAVGPAGKDGE-----AGAQGPPGP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-104-889-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (516) 228-848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1171 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 11553
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: UNIONDALE STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -AGSPGFOGLPGPA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGPPGAR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 GOMGPRGLPGERGRPGAPGPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GEPGPT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLIGSPGSPGPDGKIGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGER 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFLQGLPGPAGPPGEAGKP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGPRGEQGPAGSPGFQGLPGPAGPPGEAGKP 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .----TGLPGPP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- AGRPGEAGLP 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GPMGPSGPRGLPGPPGAPGPQGFQGPPGEPGBPGASGPMGPRGPPGPPGKNGDDGEAGKP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1107;
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                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GPSGPA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%; Score 2765; DB 15;
llarity 55.4%; Pred. No. 3.9e-131;
Conservative 31; Mismatches 228;
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-0CT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFREEY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEOGVPGDLGAPGPSGPAGE
                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TOPOLOGY: unknown | MOLECULE TYPE: peptide | SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-104-889-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1107 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
Matches 561; Conserva
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d 8 유 ò g  $\dot{\delta}$ Db δ 셤  $\delta$ 엄  $\stackrel{>}{\circ}$ В ò g ò d  $\delta$ 요 ò 셤 ò

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GPQGPGGPPGPKGNSGEPGAPGSKGDTGAKGEPGPVGVQGPPGPAGEEGKRGARGEPGPT 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGASGPMGPRGPPGFRNGDDGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOMGPRGLPGERGRPGAPGAPAGARGNDGATGAAGPPGPTGPAGPPGFPGAVGAKGEAGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRPGERGPPGPQGARGLPGTAGLPGMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPGPAGPAGERGEQGP-----AGSPGFQGLPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GRPGEAGLP---GAKGLTGSPGP-----DGKTGPPGPAGQDGRPGPPGAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192;
                                                                                                APPLICANT: GRUSKIN, ELLIOT A.
BUBCHTER, DOUGLAS
BURCHTER, DOUGLAS
BROKAW, JANE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2765; DB 15;
Pred. No. 4.6e-131;
                                                                                                                                                                                                                                                                ADDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,889
FILING DATE: 22-Mar-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 31, Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-104-889-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEEN, JEFFREY S
TELECONTULICATION INFORMATION:
TELEPHONE: (516) 228-8484
TELEFAX: (516) 228-8516
                                        Sequence 10, Application US/10104889
Publication No. US20040086961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
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                                        Indels
Sinilarity 55.4%; Score 2765; DB 15; Similarity 55.4%; Pred. No. 4e-131; 1; Conservative 31; Mismatches 228;
                                                                                                                                                              GRPGEAGLP---GAKGLTGSPGSPGP----
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1079 GPAGARGPAGPAGPRGDKGETGEGGDRGIKGHRGFSGLQGPPGPPGSPGSPGGPSGASGPA 1138
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                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10358024
Publication No. US20040151732A1
GENERAL INFORMATION:
APPLICANT: Jicha, Douglas L.
APPLICANT: Pelsue, Stephen
TITLE OF INVENTION: Methods and Compositions Involving Blood
TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
FILE REFERENCE: 14436US
CURRENT APPLICATION UNMBER: US/10/358,024
CURRENT PILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                            ---AGAQGPPGP
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TYPE: PRT
ORGANISM: Homo Sapien
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US-10-358-024-1
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APPLICANT: Jicha, Douglas L.

TITLE OF INVENTION: Method and Compositions Involving
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
CURRENT APPLICATION NUMBER: US/10/357,851
CURRENT FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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US-10-357-851-1
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                                             GPRGSEGPQGVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPS
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Fublication No. US20040157329A1
GENERAL INPORMATION:
APPLICANT: ADD Pharmaceutical Pty Limited
TITLE OF INVENTION: Matrix gene expression in chondrogenesis
FILE REFERENCE: 50031.
CURRENT APPLICATION NUMBER: US/10/468,091
CURRENT APPLICATION NUMBER: AU PR3116
FRIOR APPLICATION NUMBER: AU PR3116
FRIOR FILING DATE: 2001-02-15
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GEQGVPGDLGAPGPSGARGERGFPGERGVQGPPGPAGPRGANGAPGNDGAKGDAGAPGAP
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                                                                                                                    475 GAK-----GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ------
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55.4%; Pred. No. 4.8e-131;
ive 31; Mismatches 228;
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US-10-788-792-150

US-10-788-792-150

Sequence 150, Application US/10788792

Publication No. US20040191819A1

GENERAL INFORMATION:

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Breaked, Deepa

APPLICANT: Brewood, Douglas

TILLE OF INVENTION: EXPRESSION PROFILES FOR BREAF

FILE REFERENCE: 515.2

CURRENT APPLICATION NUMBER: US/10/788,792

CURRENT FILING DATE: 2004-02-27

PRIOR APPLICATION NUMBER: US 60/450,655

PRIOR FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 254

SEQ ID NO 150
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 561; Conserv
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GERGEQGPAGSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
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                                                                                                                                                    PAPPLICANT: Hyaeq, Inc.
APPLICANT: Tang et al
TITLE OF INVENTION:
FILE PETERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-7
PRIOR FILING DATE: 2000-01-7
PRIOR FILING DATE: 2000-01-7
PRIOR FILING DATE: 2000-09-15
                                                                                                           ; Sequence 243, Application US/10291265; Publication No. US20030232054A1; GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                59.5%; Score 2761; DB 16; 55.3%; Pred. No. 7.5e-131; ive 31; Mismatches 229;
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                                                                                                     Best Local Similarity 55.3
Matches 560; Conservative
     ; LENGTH: 1461.; TYPE: PRT; ORGANISM: Homo sapiens
US-10-468-091-25
                                                                                                   Similarity
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                                                                                                                                          GRPGEAGLP---GAKGLTGSPGSPGP-----DGKTGPPGPAGQDGRPGPPGAR
                                                                                                                                                                                                                                      106 GOAGVMGFPGPKGAAGEPGKAGER-----GVPGPPGAVGPA-----GKDGEAGAQ
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959 GVVGLPGQRGERGFPGLPGPSGEPGKQGPSGASGERGPPGPMGPPGLAGPPGESGREGAP 1018
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719 GSQGAPGLQGMPGERGAAGLPGPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPGPAGAP
                                                                                                              516 ----AGVMGFPGPKGAAGEPGKAGERGVPGPPGA-----VGPAGKDGEAGAQGPP
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APPLICANT: Kales, Michael D.
APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FRRISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 159, Application US/10060036; Publication No. US20030073144A1; GENERAL INFORMATION:
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; LENGTH: 1464
; TYPE: PRT
; CRGANISM: Homo sapiens
US-10-060-036-159
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                              978 GPRGPPGSAGAPGKDGLNGLPGP1GPPGPRGRTGDAGPVGPPGPPGPPGPPG 1029
      820
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      GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG
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                                                                                                                                Sequence 261, Application US/0918715
Sequence 261, Application US/0918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad & C. Croix
APPLICANT: Brat Vogelstein
APPLICANT: Reneth Kinzler
TITLE OF INVENTION: RNOTHELIAL CELL EXPRESSION PATHERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR PILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 1464
TYPE: PRI
COGANISM: Homo sapiene
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55.2%; Pred. No. 1.5e-130;
cive 31; Mismatches 230;
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Best Local Similarity 55.2%
Matches 559; Conservative
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| 418  | 213                               | 273<br>538   | 333<br>598   | 393<br>658  | 423<br>718                     | 474   | 515<br>838                                | 561<br>898                                     | 618<br>958   | 675<br>1018   | 735<br>1078  | 771<br>1138                           |   |
|--|-----------------------------------|--|--|---|--------------------------------|---|---|--|--|---|--|---------------------------------------|---|
| GPRGSEGPOGVRGEPGPPGPAGAAGPAGNPGADGOPGAKGANGAPGIAGAPGFPGARGPS | GPPGBAGKPGBOGVPGDLGAPGBEGPAGBEGPT | GLPGPPGERGGPGSRGFPQADGVAGPKGPAGERGSPGPAGFKGSPGEAGRPGEAGLPGAK | GLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGRAGQAGVMGFPGPKGAAGEPGKAGER [ | GVPGPPGAVGPAGKDGBAGAQGPPGPAGBAGBRGEGGGPAGSPGFQGLPGPAGPPGBAGKPFGEAKP | GEGGVPQDLGAPGPSGPAGEPGPTGLPGPP | GERGGPGSRGFPGADGVAGPKGPAGERGSPCPAGPKGSPGEAGRPGEAGLP | GAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGRAGQ | AGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPP | GPAGPAGERGEDGRAGSPGFQGLPGPAGPPGEAGKPGEDGGVPGDLGAPGPSGPAGEP | GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGBRGSPGPAGPKGSPGEAGRPGEA | GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGBP | GKAGERGVPGPPCAVGPAGKDGEAGPAGSPPGPAGPA | GERGEGGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820 |
| 359  | 181                               | 214  | 539  | 334   | 394<br>659                     | 424   | 475                                       | 516<br>839                                     | 562<br>899   | 619<br>959  | 676  | 736                                   | 772   |
| qu   | oy<br>Bb                          | o,<br>P  | oy<br>B  | Qy<br>Dp  | çy<br>Dp.                      | oy oy   | Qy  | Qy   | oy<br>Dp   | , qa<br>ap  | Qy<br>Dp   | 9<br>9                                | QV<br>equ   |

Search completed: October 18, 2004, 13:58:35 Job time: 112.622 secs

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October 18, 2004, 13:31:10 ; Search time 32.5431 Seconds (without alignments) 2427.363 Million cell updates/sec
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4640
1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821
                                                                                                                                                                                                                                                                                                                                                                283416
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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                                                                      OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            | Description | agen al | lagen alpha 1( | lagen alpha 1( | agen alpha 1( | collagen alpha 1(I | alpha 1( | alpha 1( | а      | Ч      | alpha 1 | <u>_</u> | alpha 1 | alpha 2 | en type | alpha 2 | alpha 2 | alpha 1 | alpha 1 | alpha 1 | alpha 1 | collagen alpha 1(X | alpha 1 | alpha 2 | alpha cl | alpha 1 | alpha 2 | collagen alpha 5(I | alpha 4 | type VII collagen |
|------------|-------------|---------|----------------|----------------|---------------|--------------------|----------|----------|--------|--------|---------|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|--------------------|---------|---------|----------|---------|---------|--------------------|---------|-------------------|
| SUMMARIES  | di          | GHUI    |                | 딮              | T45467        | 30                 | A41182   | B41182   | B40333 | A40333 | CGBO7S  | 859856   | CGHU7L  | CGHU2V  | 149607  | A43291  | CGHU2S  | CGRT1S  | CCHUIV  | S18803  | CGBO1S  | CGHULE             | 150694  | 2380    | S28774   | A54849  | CGHUZE  | 822917             |         | 0                 |
|            | DB          | Н       | 7              | <del>,  </del> | N             | Н                  | ~        | 71       | Н      | 7      | Н       | ~        | Н       | ٦       | 7       | Н       | Н       | н       | Н       | N       | н       | н                  | ~       | Н       | ~        | ~       | Н       | rH                 | Н       | 0                 |
|            | Length      | 46      | 45             | 04             | 47            | 1487               | 41       | 48       | 48     | 49     | 04      | ø        | 46      | 49      | 49      | 37      | S       | $\sim$  | 83      | 4       | ~       | 1806               | ထ       | 41      | 2        | 94      | 1546    | 69                 | 69      | 54                |
| *<br>Ouerv | Match       | σ       | 58.9           | 7              | 53.4          | 53.4               | 53.0     | س        | 51.7   | ÷.     | ä       | 51.2     | ä       | °.      | σ.      | σ,      |         | ω.      |         | 47.6    |         | 46.7               | •       | •       | 44.7     | 44.6    | 44.4    | 44.4               | 44.1    | 43.9              |
|            | Score       | 275     | ά.             | 67             | 47            | 47                 | 46       | 46       | 0.4    | 38     | 237     | 7        | 37      | 232     | ы.      | 230     | ω.      | 223     | 229.    | œ       | 193.    | 2169               | 161.    | ġ       | 074.     | 0,7     | ö       | 05                 | 94      | 03                |
| Result     | No.         |         | 7              | ٣              | 4             | ហ                  | 9        | 7        | Φ      | σν     | 10      | 11       | 12      | 13      | 14      | 15      | 16      | 17      | 18      | 19      | 20      | 21                 | 22      | 23      | 24       | 25      | 26      | 27                 | 28      | 29                |

| 1pha      | collagen alpha 1(I | lpha   | 1pha    | 듼      | collagen alpha 2(I | Ξ      | ์      | $\Xi$  | Э      | ä      | Η      | lpha   | collagen COLF1 - f | 1pha-  | collagen alpha 6(I |
|-----------|--------------------|--------|---------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|
| S16366    | CGHU4B             | CGMS4B | CGHU3B. | 823810 | CGHU2B             | T29351 | T29350 | A45407 | S18251 | A33526 | A31893 | 840991 | 831521             | A54121 | CGHU6B             |
| ~         | H                  |        | Н       | (1     | Ч                  | 7      | N      | (1     | ~      | N      | N      | (3     | ~                  | a      | н                  |
| 1763      | 1669               | 1669   | 1670    | 1603   | 1712               | 1759   | 1758   | 1752   | 1024   | 1707   | 1775   | 1744   | 812                | 1747   | 1691               |
|           |                    | _      | 0       | σı     | 9                  | m      | ~      | Н      | σ      | 7      | m      | m      | ø                  | ιū     | 'n                 |
| 43.8      | 43.0               | 42.8   | 42      | 41.    | 41.                | 41.    | 41.    | 41     | 40.    | 40.    | 40.    | 40.    | 39                 | 39     | 39                 |
| 2030 43.8 | ١.                 |        |         |        |                    |        |        |        |        |        |        |        |                    |        |                    |

## ALIGNMENTS

| CGHOIS<br>COllag<br>N,Alte | Coliagen alpha 111) Chain precursor - numan<br>Nyalternate names: procollagen alpha 1(1) chain  |
|----------------------------|---|
| ບບົບທີ່ຂໍ                  | C.)Specials: Lodio Saplens (mail)<br>C.)Bate: 12-Mug-1981 #eequence revision 04-Oct-1996 #text change 09-Jul-2004<br>C.)Accession: I60114; 801143; A93335; I55254; A39943; I55237; A35233; 809400; B90567; S1<br>S269; A29439; I53466; A02882; I37247<br>B.D.Alacsio M. Rarnard M. Prefrontius D. I. de Wer W. Pamiror F. Drefortions D. I  |
| ধেউন নি                    | the region encompassing the first twenty-fi<br>; PMID:2843432   |
| बबंदे                      | A;Accession: 160114 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA   |
| दस्या                      | A; Resultues: 1.2-9; 1.7-1.298 (2014)<br>A; Cross-references: UNIPROT: P02452; UNIPROT: 014992; UNIPROT: 016053; UNIPROT: 013896; UNI<br>R; Tromp. G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Proc   |
| ા ત ત                      | blockers, o. 23, 213-22, 1308<br>A/Title: Structure of a full-length cDNA clone for the prepro-alpha-1(1) chain of human<br>A/Reference number: S01143; MUID:89025644; PMID:3178743   |
| AK                         | A, Molecules of the management      |
| 4 A A                      | A; MEDITURES: 1712 ALTO. A. A. A. A. A. A. CESSE-REFERENCES: MAICTOSE-REFERENCES: EMBL: X07884; NID: 930016; BID: 930016; GB: M36546; NI A; Mote: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988  |
| αž                         | R;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C<br>Nature 310, 337-340, 1984   |
| AAA                        |   |
| AA                         | A. Modecule DNA A. Modecule DNA A. Modecule DNA A. Modecule DNA A. Modecule 1 - 58 / 0/ 60-181 / 0/117  |
| ישׁ                        | A; fross-references: EMBL:X00820; NID:g35657; PIDN:CAA25394.1; PID:g35658<br>A;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W  |
| च बें बें<br>-             | u. biol. Chem. 1864, 1911-1-1877, 1984.<br>A.Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene en.<br>A.Reference number: 155254; MUID:88033098; PMID:2822714  |
| d d a                      | A;Accession: 155254<br>A)Status: translation not shown; translated from GB/EMBL/DDBJ<br>A:Wolevile trans. DNS   |
| દર્લ                       | A.mosiduss: 1.45 < ROS>   |
| 4 2 6                      | A,Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388<br>R:Bornstein, P.; McKay, J; Mortishiam, J.K.; Devardyalu, S.; Gelinas, R.E.<br>Proc. Natl. Acad. Griff, B. 24. Asseq-RR73, 1987, |
| AAA                        | A; Title: Regulatory elements in the first intron contribute to transcriptional control A; Reference number: A39943; MUID:88097389; PMID:3480516  |
| दिवदेष                     | A;NOCCEDEL TYPE: DNA<br>A;NOCEDULE 1798: DNA<br>A;Rossidues: 1-34 <bors-<br>A;Cross-references: GBS-<br/>A;Cross-references: GBS-<br/>R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.</bors-<br>  |

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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Mostuces: 425-1250, X',1252-1328, S',1330-1390, X',1332-1464 <BER>
A.Gross-references: GB:KO1228, NID:g180391; PIDN:AAA51995.1; PID:g180392
A.Note: sequence partially completed for missing nucleotides by A29439
A.Note: sequence partially completed for missing nucleotides by A29439
A.Note: Sequence partially williams, C.J.; Ramirez, F.
J. B.Ool. Chem. 260, 691-694, 1995
A.Title: Miltiexon deletion in an osteogenesis imperfecta variant with increased type II
A.Reference number: A22161; MUID:85104934; PMID:2981843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: A35336
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A.Molecule type: mRNA
A.Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A.Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A.Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A.Note: the authors 22012206, 1994
Hum. Mol. Genet. 3, 22012206, 1994
A.Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the C
A.Reference number: I54365, MUID:95187161, PMID:7891420
        A,Accession: I52905
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A,Status: translated from GB/EMBL/DDBJ
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A,Cross-references: GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:g408196
B,Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
Biochemistry 22, 5213-5223, 1983
A,Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A,Reference number: A90476; MUID:84080385; PMID:6689127
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A; Residues: 1179-1387, R', 1389-1464 <CH7>
A; Experimental source: fetal cell 88-551
R; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Ni
J. Biol. Chem. 253, 14650-1460-1, 198
A; Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide
A; Reference number: 155269; MUID:89008319; PMID:3170557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EWBL/DDBJ
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A;Residues: 746-766, 531 < FOR>
A;Cross-references: GB:L47667; NID:g1009093; PIDN:AAB59576.1; PID:g1009094
B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J Biol. Chem. 268, 18218-18225, 1993
A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of A;Reference number: A47426; MUID:93352646; PMID:9349697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: mRNA;
;Residues: 1179-1276, 'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
;Cross-references: GB:864596; NID:9407589; PIDN:AAB27856.1; PID:9407590
;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
;Note: does not represent an experimentally determined sequence but three different;Accession: B47426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1179-1464 <CH4>
Experimental source: normal dermal fibroblast culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A35336; MUID:90252792; PMID:2339700
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:Residues: 1179-1276,'H',1278-1464 <CH5>
:Experimental source: fetal cell 86-237
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A;Experimental source: fetal cell 86-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 472-594,'R',596-607 <CH3>
                                                                                                                                                                                                                                                                                                        A; Accession: A90476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A22161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I54365
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A/Molecule type: DNA
A/Cross-references: GB:M10627; NID:g180383; PIDN:AAA51992.1; PID:g553226
B;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
B;Wirtz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
A/TILle: In vivo and in vitro noncovalent association of excised alphal(I) amino-termina
rome, type VII.
A/Reference number: A35233; MUID:90202908; PMID:2318855
J. Biol. Chem. 260, 2315-2320, 1985
A/Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter
A;Reference number: 155237; MUID:85130970; PMID:2857713
A;Accession: 155237
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 33-52 <WIR>
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| A. Stetute Translated from GRYDMAL/DOUGH.  A. Mosterule Type: 1187-1194. C. 1136-1219. CORP.  A. Residence Commission and December 1187-1194. C. 1136-1219. CORP.  A. Residence Commission and December 1187-1194. C. 1136-1219. CORP.  A. Title: Imman pro-alpha-1(1) collegen: Did on top of the C-propertide domain.  A. Title: A minimal pro-alpha-1(1) collegen: Did on top of the C-propertide domain.  A. Title: A minimal pro-alpha-1(1) collegen: Did on top of the C-propertide domain.  A. Title: A minimal pro-alpha-1(1) collegen: Did on top of the C-propertide domain.  Bearly March S. Title: A minimal pro-alpha-1(1) collegen: Did on top of the C-propertide domain.  Barry March  Ba | 8 8 8  | 3  | SEST<br>S210<br>COL   | O O O O O O O O O O O O O O O O O O O                          | हुत्य<br>स्थ्रं                                 | 44444   | TAAAA                           | A A A A                               | A P G P F F F F F F F F F F F F F F F F F                           | 4444   | A A A A   | I A A A                            | CRU K   | द्वद्वद                                      | A W W W  | 4444   | A W W W   | 44444  |
|--|--|--|---|--|---|---|---------------------------------|---------------------------------------|---|--|---|------------------------------------|---|--|--|--|---|--|
|  | translated from GB/EMBL/DDBJ<br>e type: DNA<br>ss: 1187-1194,'C',1196-1220 <coh><br/>teferences: GB:M23213; NID:g340842; PIDN:AAB59363.1; PID:g49962<br/>utant sequence from a patient with mild osteogenesis imperfect<br/>e, J.K.; Raassina, M.; Virta, A.; Vuorio, E.</coh> | cids kes. 16, 349, 1988<br>Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide | tch samilarity 59.4%; Score 2756; DB 1; Length 1464; sal Similarity 55.3%; Pred. No. 3.5e-130; S60; Conservative 31; Mismatches 229; Indels 192; Gaps 1 | 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGBA 57 | 58 GRPGEAGLPGAKGLIGSPGSPDGKTGPPGPAGQDGRPGPPGARR | 106 GQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAO | 151 GPPGPAGERGEQGPAGSPGFQGLPGPA | 181 GPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPT | 214 GLPGPPGERGGPGSRGFPGADGVAGPKGPRGERGSPGPAGPKGSPGEAGRPGEAGLPGAK 27 | 274 GLIGSPGSPGFPGFPGPPGPPGPPGPAGGAGWAFFGPKGAAGER33<br> | 334 GVPGPPGAVGPAGKDGBAGAQGPPGPAGFAGERGEQGPAGSPGFQGLPGPAGPPGBAGKP 39 | 394 GEQGVPGDLGAPGPSGPAGEPGPTGLPGPP | 424 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGBAGRPGEAGLP 47. | 475 GAKGLTGSPGSPGPDGKTGPFGPAGQDGRPGPPGARGQ51 | 516AGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 56 | 562 GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGBQGVPGDLGAPGPSGPAGEP 61 | 619 GPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGFKGSPGEAGRPGEA 675 | 676 GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP |

| Cross-references: EMBL:X54876; NID:g50486; PIDN:C<br>Genetics:<br>Gene: COL1A1  | :    :    :  |
|---|--|
| A)Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/<br>C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;<br>C;Keywords: coiled coil: extracellular matrix; glycoprotein; heterotrimer; triple helix<br>F;1-22/Domain: signal semience Herarus machine controlled. | OY 747PGAVGPAGKDGEAGAQGPPGPAGPAGSPGBAGSP 783  Db 1080 GPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGGPSGASGPAGPRGPGSAGSP 1139   |
| 23-151/Domain: amino-terminal propertide fratus<br>30-89/Domain: von Willebrand factor type C repeat<br>152-1453/Product: collagen alpha 1(I) chain #stat<br>1224-1453/Domain: fibrillar collagen carboxyl-ter  | QY 784GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820<br>  |
| Ouery Match 58.9%; Score 2732.5; DB 2; Length 1453;<br>Best Local Similarity 54.7%; Pred. No. 5.1e-129;<br>Matches 547; Conservative 33; Mismatches 240; Indels 180; Gaps 16;   | RESULT 3<br>CGCHIS<br>collagen alpha 1(I) chain - chicken (tentative sequence) (fragments)   |
| QY 1 GPPGEBGPTGLPGPPGERGGPGSRGFPGADGVAGPKGFAGERGSPGPA 48  | C.Species: Gallus gallus (chicken)<br>C.Jate: 12-Aug-1981 #sequence revision 06-Jul-1982 #text_change 31-Mar-2000<br>C.Accession: A90458, A90181; A02857<br>R.Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Sever, J.M.; Kang, A.H.: Gross. J  |
| QY 49 GPKGSPGEAGRPGEAGLPGAKGLIGSPGSPGPDGKTGPPGPAGQD 93  | lagen alphal(I)-CB8 and the complete pri<br>D:7093229  |
| QY 94 GRPGPPGARGQAGWMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEA 147   | A, Molecule type: protein<br>A, Residues: 1-1036 <htg><br/>A, Experimental source: skin<br/>A, Note: this is the latest in a series of papers from these workers elucidating the semi</htg>  |
| QY 148 GAQGPPGPAGBAGBRGBQGPAGSPGFQGLPGPAGPPGEAGKPGEQ 192  | 72<br>sequence at the carboxyterminus of the<br>D:5047697  |
| QY 193 GVPGDLGAPGPSGPAGBPGPTGLPGPPGERGGP 225  | A;Accession: A90181 A;Molecule type: protein A;Esidues: 1037-1042 < EYR> A;Experimental source: stin   |
| Qy 226 GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285   | A; Note: residues 1037-1042 above correspond to the carboxyl end of the protein C; Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in some C; Comment: Most of the prolines at the third position of the tripeptide repeating unit (C; Comment: Pro-1002 is the only 3-hydroxynchine and the only hydroxylated nooline in |
| SPA<br>   | illar collagen carboxyl terminal homolog<br>glycoprotein; pyroglutamic acid; trimer<br>(Gln) #status experimental  |
|   | Query Match 57.7%; Score 2679; DB 1; Length 1042;<br>Best Local Similarity 53.7%; Pred. No. 1.8e-126;<br>Matches 540; Conservative 30; Mismatches 250; Indels 186; Gaps 16;  |
|   | OY 1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPRGPAGER 42   |
| 84 7  | QY 43 GSPGPAGPKGSPGEAGRPGEAGKGLPGSPGSPGPDGKTGPPGPAGQD 93   |
| . το α  | Qy 94GRPGPPGRPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA 141  Db 143 GLPGERGRPGPSGPAGARGNDGAPGAAGPPGPTGPAGPPGPAGAKGETGPQGARGSE 202  |
| GPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGER 57   | Qy         142 GKDGEAGAQGPPGPAGPRGEQGPAGSPGFQGLPGPAGPPGEA 186           L  |
| GEQGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGTFGLPGPPGER  | Cy 187 GKPGECGVPGDLGAPGPSGPAGEPGPTGLPGPP 219   |
| 687   | OY 220 GERGGPGSRGFPGADGVAGPKGFAGFRGSPGFAGPKGSFGEAGLPGAKGLIGSP 279  |
| 9 8 9   | Qy 280 GSPGPDGKTGPPGPAGQDGRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP 339   |

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Bur. J. Blochem. 234, 125-131, 1995
A; Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil car A; Accession: 863514; MUID: 96096730; PMID: 8529631
A; Accession: 863514
A; Molecule type: protein
A; Residues: 243-261;575-590;756-763, X, 765-779 < FRA>
K; Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre, Am. J. Hum. Genet. 56, 388-395, 1995
A; Titler, A: AR RAPA splicing mutation (G+51VS20) in the type II collagen gene (COLZA1) in a A; Accession: 138867; MUD: 95150028; PMID: 7847372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 630-640, 'A', 642-785 «VIKZ»
A; Cross-references: EMBL:X16158; NID:92951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3428
PIDN:CAA34283.1; PID:91335023; PIDN:CAA34284.1; PID:91335024
R; Bogaert, R.; Tiller, G.E.; Weis, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Byre, D.A.; Biol. Chem. 267, 22526-2256, 1992
A; Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain pro
A; Reference number: A44309; WUID:93054548; PMID:1429602
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A;Titler Tandem duplication within a type II collagen gene (COL2A1) exon in an individua A;Reference number: S16502; MUID: 90251662; PMID: 2339128
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A; Residues: 1164-1184, GPSGKDGANGIPGPI',1185-1199 <TILZ>
A; Cross-references: EMBL:M37126; NID:g180809; PIDN:AAAS2037.1; PID:g180809
A; Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R; Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
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A; Title: Identification and characterization of the human type II collagen gene (COL2A1)
A; Reference number: A02858; MUID:85190534; PMID:3857598
                     P.; Herbage,
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A; Residues: 1175-1487 <ELIS
A; Cross-references: BMBL:X06268; NID:g30096; PIDN:CAA29604.1; PID:g30097
A; Experimental source: fetal epiphyseal cartilage
R; van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
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A; Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type II collagen gene
        S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 440,'G',42-456,'E',458-480,'P',482-509 <TILL>
A;Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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A,Residues: 501-676, A', 678-783, A', 785-831, PA', 834, F', 836-1214 <RAM>
A,Gross-references: EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PID:g930050
R,Vikkula, M.; Pelconen, L.
R,Vikkula, M.; Pelconen, L.
A;Title: SEructural analyses of the polymorphic area in type II collagen g
A,Reference number: S05000; WUID:89325561; PMID:2753125
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A; Residues: 1032-1056, Nv, 1058-1068, Tr, 1070-1487 < CHE>
A; Cross-references: GB: J00116; NID: g180395; PIDN: AAA51997.1;
R; Elima, K: Vuorio, T.; Vuorio, E.
Nucleic Acids Res: 15, 9499-9504, 1887
A; Title: Determination of the single polyadenylation site of
A; Reference number: A27280; MUID: 88067771; PMID: 2825137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, December 1988
A,Reference number: S04892
A,Accession: S04892
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A; Residues: 440,'G',4
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A,Molecule type: protein
A,Residues: 188-189,'X',191-195,1224-1230,'X',1232-1236 <DIA>
number: A38513; MUID:91184811; PMID:2081599
                                                                             A;Molecule type: DNA
A;Residues: 1-103 <RYA>
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collagen alpha 1(II) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: 28-May-1992 #text_change 13-Aug-1999
C;Accession: A41182; A44885
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
J. Biol. Chem. 266, 16862-16869, 1991
A;Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A;Reference number: A41182; MuID:91358489; PMID:1885613
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A; Readudes: 1.1419 < MET>
A; Cross-references: GB: M65161
A; Cross-references: GB: M65161
B; Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
Development 111, 946-953, 1991
A; Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartila, A; Reference number: A44885; MUID: 91347939; PMID: 1879363
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A,Residues: 1-28 <CHE>
A,FResidues: 1-28 <CHE>
A,COCES references: GB:S63190, NID:g234368, FIDN:AAB19627.1; PID:g234369
A,NOCE: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
C,Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
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                                                                                                                  357
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                                                                                                                                                                                                                                                                            358 GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 GETGPPGTSGIAGPPGADGQPGAKGEQGBAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 884
                                      525 GPKGAPGERGPSGLAGPKGANGDPGRPGLPGARGLTGRPGDAGPQGKVGPSGAPGED 584
                                                                                                                       GRPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP
                                                                                                                                                                     685 GSPGSPGPDGKTGPPGP-----AGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
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793 GPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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                         A,Acceston: AS7033
A,Acceston: AS7033
A,Molecule type: protein
A,Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prop
A,Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prop
R,Strom, C.M.; Uppoll, W.B.
A,Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal prop
R,Strom, C.M.; Uppoll, W.B.
A,Ittle: Isolation and characterization of genomic clones corresponding to the human typ
A,Reference number: A21733; MUD:84118798; PMID:6320112
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A,Molecule type: DNA
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A,Accession: B21733
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A,Residues: B94-909, PE' cSTR2>
A,Cross-references: GB:KC01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A,Cross-references: GB:KC01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A,Cross-references: GB:KC01785; NID:g30035; PIDN:CAA25082.1; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A,Title: Isolation and partial characterization of genomic clones coding for a human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A24561; MUID:86104139; PMID:3002437
A; Accession. A24561; MUID:86104139; PMID:3002437
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A; Residues: 1296-1358 «NUM2>
A; Cross-references: GBM12048; MID:g180017
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the A; Sandjorg1, F.O.; Benson-Chanda, V; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez, Nucleic Acids Res. 13, 2207-2225, 1985
A; Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll A; Reference number: 137249; MUID:85215609; PMID:2987845
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A;Residues: 7-28;R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1
A;Accession: 184453
A;Accession: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 7-28 <SAN2>
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A;Note: the GenBank PID is based on an incorrect reading frame
A;Status: 137250
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 541-560 cSAN3>
A,Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A,Accession: 137251
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Best Local Similarity 50.9%; Pred. No. 2.7e-116;
Matches 503; Conservative 45; Mismatches 272; Indels 168; Gaps 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 -----GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 GASGNPGTDGIPGAKGSAGAPGIAGAPGFPGPRGPPDPQGATGPLGPKGQTGKPGIAGFK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GPPGERGGPGSRGFPGADGVA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 GNPGEPGEPGVSGPMGPRGPPGPPGKPGDDGEAGKPGKAGERGPPGPQGARGPFGTPGLP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 GQDGRPGPPGPPGARGQAGVMGFP-----GPKGAAGEPGKAGERGVPGPPGAVGPA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 GNDGQPGPAGPPGPVGPAGGPGPPGAPGAKGEAGPTGARGPEGAQGPRGEPGTPGSPGPA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
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Reference number: A57033; MUID:87099927; PMID:3800925
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Species: Ms. Microlina, Microlina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGE---- 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGSRGEPGNPGSPGPA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 GKDGE-----AGSPGFPGFAGFAGFRGEQGP-----AGSPGFQGLP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRPGPPGPQGARGOPGVMGFPGPKGANGEPGKAGEKGLAGAPGLRGLPGKDGETGAAGPP 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASGNPGTDG1PGAKGSAGAPG1AGAPGFPGPRGPPGPQGATGPLGPKGQAGEPG1AGFK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             705 GERGSPGAQGLQGPRGLPGTPGTPGPKGAAGPDGPPGAQGPPGLQGMPGERGAAGIAGPK 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AGRPGEAGLPGAKGLTGSPGSPGPD 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765 GDRGDVGEXGPEGAPGKDGGRGLTGPIGPPGPAGANGEXGEVGPPGPSGSTGARGAPGEP 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GETGPPGPAGFAGPPGADGQPGAKGDQGBAGQKGDAGAPGPQGPSGAPGPQGPTGVTGPK 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Mismatches 271; Indels 168; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1487;
                                                                                                                                                     collagen alpha 1(II) chain precursor (long splice form) - mouse
C,Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.0%; Score 2460; DB 2; 50.6%; Pred. No. 1.7e-115;
1117 GPPGPRGRSGETGPVGPPGSPGPPG 1144
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Best Local Similarity 50.6
Matches 500, Conservative
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C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime
F;1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAPGAPGPPGSPGPAGPTGKQGDRGEAGAQGPMGPSGPAGARGIAGPQGPRGDKGESGEQ 1056
                                                                                                                                                                                                                                                         GNPGEPGEPGVSGPMGPRGPPGPAGKPGDDGEAGKSGERGLPGPQGARGFPGTPGLP 216
                                                                                                                                                                                                                                                                                                                                                                                                    217 GVKGHRGYPGLDGAKGEAGAPGVKGESGSPGENGSPGPMGPRGLPGERGRTGPAGAAGAR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GERGVPGPPGA-----VGPAGKDGEAGAQGPPGPA---GPAGERGEQGPAGSPGFQ 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPGSPGPDGKTGPPGP-----AGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GODGRPGPPGARGOAGVMGFP-----GPKGAAGEPGKAGERGVPGPPGAVGPA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNDGQPGPAGPPGPVGPAGGPGFPGAPGAKGEAGPTGARGPEGAQGSRGEPGNPGSPGPA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKDGE-----AGSPGGPPGPAGPAGERGEQGP----AGSPGFDGLP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 GASGNPGTDGIPGAKGSAGAPGIAGAPGPPGPRGPPGPQGATGPLGPKGQAGEPGIAGFK 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 GRPGPPGPPGARGÓPGVMGFPGPKGANGEPGKAGEKGLAGAPGLRGLPGKDGETGÁAGPP 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPAGPAGERGEQGPAGSPGFPGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE---- 413
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                                                                                             Length 1419;
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                                                                                         53.0%; Score 2460; DB 2; I
50.6%; Pred. No. 1.6e-115;
live 49; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                            --GEAGLPGAKGLTGSP---GSPGP-
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| Db   | 885 GARGAQGPPGATGFPGAAGRVGPPGANGNPGPAGPPGPAGKDGPKGVRGDSGPPGRAGDP 944   | qa   | 569 GDAGPQGKVGPSGASGEDGRPGPPGPQGARGQPGVMGFPGPKGANGEPGKAGEKGLVGAP 628  |
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| දුරු   | 583 GLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGAD 642   | <i>ò</i> 6                                     | 340 GAVGPAGKDGEAGAQGPPGPAGPAGBRGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVP 399  |
| çy<br>Dp   | 643 GVAGPKGPAGERGSPGPAGPKGSPGEAGLPGAKGLT 684   | & <del>Q</del>                                 | 400 GDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPA 456   |
| 55 GG  | 685 GSPGSPGPDGKTGPPGPAQQDGRPGPPGARQQAGVMGFPGPKGAAGEP 735 1065 GAPGAPGPPGSPGPAGPTGKQCDRGEAGAQGPMGPSGPAGARGIAGPQGPRGDKGSSGEQ 1124  | \$ 6<br>6                                      | 457 GPKGSPGBAGRPGEAGLPCAKGLTGSPGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPCARGQA 516<br>   |
| oy<br>Oy   | 736 GKAGERGVPGPPGAVGPAGKDGEAGAAQGPPGPAGPAGPAGSPAGSPGFQGLPGPA 792<br>   | y du   | 517 GYMGFPGPKGAAGEPGKAGERGVPGPPGAVGPACKDGEAGAQGPP 561   |
| රු සි  | 793 GPPGEAGKPGEGGVPGDLGAPGPSGPAG 820   | QV<br>Dp                                       | 562 GPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKP 597  |
| RESULT 8 B40333 Colladen 6 Colladen 6 Colladen 7 Collad | RESULT 8  49.033  collagen alpha 1(II) chain precursor - African clawed frog  collagen alpha 1(II) chain precursor - African clawed frog  collagen alpha 1(II) chain precursor - African clawed frog  cypete: 10-Sep 1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004  cylacession: Bull 115 155-575, 1991  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis en  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis en  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis en  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis  Ayritle: Expression of two nonal-lic type II procollagen genes during Xenopus laevis  Ayritle: Expression of two nonal-lic type II procollagen genes  Ayritle: Expression of two nonal-lic type II procollagen genes  Ayritle: Expression of two nonal-lic two laevis II developed Collagen alpha III chain if the III are collagen carboxyl-terminal homology;  Cyrwords: collagen alpha III chain, fibrillar collagen carboxyl-terminal homology;  Cyrwords: collagen alpha III chain, fibrillar collagen carboxyl-terminal homology;  Cyrwords: collagen alpha III chain if the III collagen carboxyl-terminal homology;  Cyrwords: collagen alpha III collagen carboxyl-terminal homology;  Cyrwords: collagen alpha III collagen carboxyl-terminal homology;  Ayroprords: collagen alpha III collagen III co | UV<br>Db Db D | GEKGEPGEDGPPGPPGGLSGG GVAGPRGPAGERGSPGPPGPPGGLSGG GUTGSPGSPGPGPCTGPPGPAGDGG GLTGSPGSPGPDGKTGPPGPAGDGG GLTGSPGSPGPDGKTGPPGPAGDGG GLTGSPGSPGPDGKTGPPGPAGDGG GLTGSPGSPGPDGKTGPPGPAGDGG I |
| g &  | GSPGPDGKTGPPGPAGQGGRPGPRAGQAGWGFPGPKGAAGEPGKAGERGVPGPP   | qq   |   |

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Cippedies: Bos primingenius taurus (cattle)
Cippedies: Bos primingenius taurus (cattle)
Cipate: 04-Dec-1986 #sequence-revision 04-Dec-1986 #text_change 09-Jul-2004
Cipate: 04-Dec-1986 #sequence-revision 04-Dec-1986 #text_change 09-Jul-2004
Cipatesesion: A02862; A38001; A38002; A38004; A38004; A38005; S71946
Riffetzek, P.P.; Allmann, H.; Rauterberg, U.; Henkel, W.; Wachter, E.; Kuehn
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-220, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino
A;Reference number: A02862; MUD:80026026; PMID:488906
A;Accession: A02862
A;Molecule type: protein
                       GSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVM
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A. Accession: A38005, MULD: 80025031; PMID: 488911
A. Accession: A38005
A. Molecule type: protein
A. Molecule type: protei
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A; Modecule type: protein
A; Residues: 423-571 < REN>
R; Lang, H; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A; Title: The covalent structure of calf skin type III collagen. IV.
A; Reference number: A38003; MUID:80026029; PMID:488909
A; Accession: A38003
A; Molecule type: protein
A; Residues: 572-860 < LAN>
A; Residues: 572-808 < LAN>
A; Title: The covalent structure of calf skin type III collagen. V.
A; Reference number: A38004; MUID:80026030; PMID:488910
A; Reference number: A38004; MUID:80026030; PMID:488910
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A,Residues: 809-947 <DEW2>
R,Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A,Title: The covalent structure of calf skin type III collagen.
A,Reference number: A38005; MUID:80026031; PMID:488911
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                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 243-422 <DEW1>-
R,Bentz, H.; Fletzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A,Title: The covalent structure of calf skin type III c
A,Reference number: A38002; MUID:80026028; PMID:488908
                             R.Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Ghem. 360, 821-832, 1979
A.fitle: The covalent structure of calf skin type III c
A.Reference number: A38001; MUID:80026027; PMID:488907
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al Similarity 49.8%; Pred. No. 1.4e
479; Conservative 48; Mismatches
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A; Cross-references: UNIPROT: P04258
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Gigenetics:
Ainterons: 29/1; 95/3; 112/3; 150/3; 115/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 2
Ainterons: 29/1; 95/3; 112/3; 150/3; 778/3; 796/3; 814/3; 850/3; 868/3; 940/3; 976/2; 802 erfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology cysepwords: colled coll; extracellular matrix
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-154/Domain: signal sequence #status predicted <PRO>F;25-154/Domain: orn Willabrand factor type C repeat homology <WWC>
F;155-1464/Product: collagen alpha 1(II) chain #status predicted <MAT>F;125-1464/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                  A Molecule type: DNA
A;Readdues: 1-866, (9., 868-1464 < TOA>
A;Readdues: 1-866, (9., 868-1464 N. MD:9575321; PIDN:CAA36279.1; PID:9575322
A;Cross-references: EMBL:X52046; N. MD:9575321; PIDN:CAA36279.1; PID:9575322
R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biophyse. Acta 1089, 241-243, 1991
A;Title: Specific hybridization probes for meuuse type I, II, III and IX collagen mRNAs A;Title: Specific hybridization probes; PMID:2054384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 GRPGRPGERGLPGPPGIKGPAGMPGFPGMKGHRGFDGRNGEKGETGAPGLKGENGLPGDN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 GAPGPMGPRGAPGERGRP---GLPGAAGARGNDGARGSDGQPGPPGPPGTAGFPGSPGAK 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GPPGPPGARGQAGVMGFPGPK---GAAGEPGKAGERGVPGPPGAVGPA---GKDGEA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 GARGPPGPAGTNGIPGTRGPSGEPGKNGAKGEPGARGERGEAGSPGIPGPKGEDGKDGSP 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 GEVGPAGSPGSNGSPGQRGEPGPQGHAGAQGPPGPPGNNGSPGGKGEMGPAGIPGAPGLI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEPGFTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 GEPGANGLPGAAGERGPSGFRGPAGPNGIPGEKGPPGERGGPGPAGPRGVAGEPGRDGTP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X57983; NID: G50476; PIDN: CAA41048.1; PID: G50477
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                                                                                                                                      submitted to the EMBL Data Library, November 1994
        A;Accession: S59856
A;Molecule type: DNA
A;Residues: 1-1464 <TOM>
A;Cross-references: UNIPROT:P08121; EMBL:X52046
R;Toman, D.
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les 477; Conservative
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                                                                                                                                                                   A; Reference number: S62120
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C.Species: Mus musculus (house mouse)
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
R.Johnan, P.D.; de Crombrugghe, B.
Gene 147, 161-168, 1994
A.Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete
A.Reference number: $59856; MUID:95011609; PMID:7926795
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                                                                                                                                                             148 GAQGPPGPAGBAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPA 207
                                                                                                                                                                                                                  255 GARGPPGPPGTNGVPGQRGAAGEPGKNGAKGDPGPRGERGEAGSPGIAGPKGEDGKDGSP 314
                                                                                                                                                                                                                                                                       208 GEPGPTGLPGPPGERGGPGSRGFPGADGVAGPXGPAGERGSPGPAGPKGSPGBAGRPGBA 267
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GAPGPMGPRGAPGERGRP---GLPGAAGARGNDGARGSDGQPGPPGTAGFPGSPGAK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 GPPGSSGAPGKDGPPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPOGPPGAPGPLGIA 794
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                                                                                       435 GKNGERGGPGGPGPQGPAGKNGETGPQGPPGPTGPSGDKGDTGPPGPGGLQGLPGTSGPP
                                                          -----GAVGPA---GKDGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                     375 GGPGLRGIPGSPGGPGSNGKPGPPGSQGETGRPGPPGSPGPRGQPGVMGFPGPKGNDGAP
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                                                       103 GARGQAGVMGFPGPKGAAGEPGKAGERGVPGPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 -----GPPGAVGPAGKDGEAGAQGPP---
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R.Seyer, J.M.; Kang, A.H.
Jachdemistry 16, 1189-1164, 1977
A.Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A.Reference number: A90399; MUID:77134724; PMID:557335
                                                   A; Molecule type: mRNA
A; Residues: 149-163, 'G', 164-240,'D', 242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,
A; Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: IS1868; MUID:93304430; PMID:8317500
A; Accession: IS1868
A; Accession: IS1868
A; Astarus: preliminary; translated from GB/EMBL/DDBJ
A; Astarus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 186-194 < MIL>
A; Residues: 186-194 < MIL>
A; Choso-A, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1955
A; Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A; Reference number: S59511; MUID:96067614; PMID:7487954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galack
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A;Notecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: 53-66 < LES-
A;Cross-references: 63-MS9312; NID:g180815; PIDN:AAA52041.1; PID:g180816
B;Seyer, J.M.; Mainardi, C.; Kang, A.H.
B;Seyer, J.M.; Mainardi, C.; Kang, A.H.
B;Seyer, J.M.; Mainardi, C.; Kang, A.H.
A;Hitle: Covalent structure of collagen: amino acid sequence of alphal (III)-CBS from ty
A;Reference number: A90438
A;Accession: A90438
A;Accession: A90438
A;Molecule type: protein
A;Reaidues: 728-895, A, 897-964 <SBY4>
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: liver
A;Note: author submitted corrections to A90399
B;NIlewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.H.M.; Char
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A;Residues: 861-1015 <CCL>
A;Cross-references: GB:UG5617; GB:M55603; GB:M59227; NID:g180878; PIDN:AAB59383.1; PID:q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: mRNA
;Residues: 302-423 <CHI>
;Cross-references: GB:S79877; NID:g1195576; PIDN:AAB35615.1; PID:g1195577
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J. Biol. Chem. 255, 17070-17077, 1990
A; Fitle: A base substitution at a splice site in the COL3Al gene causes
A; Reference number: A38303, MUID:91009133; PMID:2145268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,Molecule type: protein
,Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Experimental source: liver
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Bloodemistry 17, 3404-3411, 1978
A.Hitle: Covalent structure of collagen: amino acid sequence
A.Reference number: A90414; MUID:79000343; PMID:687591
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,Residues: 399-675,'N',677-727 <SEY3>

,Experimental source: liver

;Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.;

Ball. Chem. 266, 5256-5259, 1991

;Title: G to T transversion at position +5 of a splice

,Reference number: ISS349; MUD:91161621; PMID:1672129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Reference number: A94562

*Molecula to A94562
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                                                                                                                                                                                                                                                                                                                                                                                   Accession: A90399
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A; Molecule ----
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Subziz; Sude4z; PE0011; S01726; S04887; A90399; A94562; IS1868; S59511; A90
R. Procksop, D. J.
Submitted to the EMBL Data Library, February 1989
A. Reference number: S0572
A. Reference number: S0572
A. Residues: L. 1240, V. V. 1242-1466 PEC>
A. Roll and A. Residues: L. 1240, V. V. 1242-1466 PEC>
A. Roll and A. Residues: L. Schuusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
B. A. Title: Structure of CDNA Clones coding for the entire prepro-alpha1(III) chain of huma A. Reference number: S0442; MUID: 89350838; PMID: 2764886
A. A. Residues: L. Soffett MID: 89350838; PMID: 2764886
A. A. Residues: S0442; MUID: 89350838; PMID: 2764886
A. A. Residues: L. Soffett MID: Residues: Reference number: Soffett MID: Reference number: Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ollagen alpha 1(III) chain precursor - human
;Alternate names: procollagen alpha 1(III) chain
;Becies: Hemo sapiens (man)
;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 09-Jul-2004
;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; IS1868; S59511; A90
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A; Residues: 1-170 <TOM>
A; Residues: 1-170 <TOM>
A; Coss-references: EMBL: X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061
A; Note: the authors translated the codon CAG for residue 154 as His
A; Vaneczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A; Reference number: S04887; MUID:89386015; PMID:2780304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1052 GPVGPSGKSGDRGETGPAGPSGAPGPAGARGAPGPQGPRGDKGETGERGSNGIKGHRGFP 1111
                                                                                                                                        GAPGQNGEPGAKGERGAPGEKGBGGPPGPPGPAGPTGSSGPAGPPGPPGPGVKGERGSPGPPGTA 871
                                                                                                                                                                                                                                                                                                                       872 GFPGGRGLPGPPGNNGNPGPPGPSGAPGKDGPPGPAGNSGSPGNPGIAGPKGDAGQPGEK 931
                                                                                                                                                                                                                                                                                                                                                                                                                     -- PGPAGQDGRP 708
GP---RGPAGPIGPPGP---AGOPGDXGEGGSPGLPGIAGPRGGPGERGEHGPPGPAGFP 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                           932 GPPGAQGPPGSPGPLGIAGLTGARGLAGPPGMPGPRGSPGPQGIKGESGKPGASGHNGER 991
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                                                                                     -----GPAGERGEQGPAGSPGFQGLPGPAGEPGE---AGKPGEQGVPGDLGAPGPSGPA
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D.

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F;154-167/Region: amino-terminal nonhelical telopeptide
F;168-1196/Region: helical
F;168-1196/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: cell attachment (R-G-D) motif
F;1222-1466/Domain: fibrilar collagen carboxylic attachment (R-G-D) motif
F;122-1466/Domain: fibrilar collagen carboxylic acid (Gln) (in mature form) #status predicte
F;124/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;151-1212/Modified site: allysine (Lys) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Reinding site: carbohydrate (Lys) (covalent) #status experimental
F;84,1094/Modified site: Gly-Ile (Collagenses) #status experimental
F;948-949/Cleavage site: Gly-Ile (Collagenses) #status experimental
F;106/Binding site: carbohydrate (Lys) (covalent) #status predicted
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A; Residues: 1165-1196 CEMA>
A; Residues: 1165-1196 CEMA>
A; Residues: 1165-1196 CEMA>
A; Cross-references: GB: MI1134; NID:g180417; PIDN:AAAS2004.1; PID:g180418
B; Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A; Title: Isolation of CDNA and genomic clones encoding human pro-alphal(III) collagen. B
A; Recession: A92516
A; Rocession: A92516
A; MulD:85157600; PMID:2579949
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 1358-1466 < CHU>
A; Residues: 1176-1240, VV, 1242-1356, PV, 
A;Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn R;Mankoo, B.S.; Dalgleish, R.
Nucleic Acids Res. 16, 2337, 1988
A;Fitle: Human pro alphal(III) collagen: cDNA sequence for the 3' end.
A;Feternce number: S02119; MUID:88189827; PMID:3357782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Modecule type: protein
A; Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096,'P', 1098-1152,'AT', 1155,'S', 1157-
A; Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096,'P', 1098-1152,'AT', 1155,'S', 1157-
A; Experimental source: liver
R; Looidl, HR.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye
Nucleic Acids Res. 12, 9383-9394, 1984
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
A; Reference number: A93551; MUID: 85087944; PMID: 6096827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross_references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A;Reference number: 159025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Map position: 2431-2431
A, Introns: 2711: 94(3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A, Introns: 2711: 94(3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A, Note: the list of introns is incomplete; defects in this gene can result in Shlers-Dan C; Complex: type III collagen is a homotrimer of monomers initially linked by disulfide be er of their length, is formed with desmosine cross-links made from lysine and allysine r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1
R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately modulated with the type A;Accession: 152393; MUID:86187804; PMID:3754462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of alphal (III) -CB9 from ty
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                                                                                                                                                                                                                                                                                                                 A; Modecule type: mRNA
A; Residues: 950-1018, 'Y', 1020-1183,'S', 1185-1466 <MAN>
A; Residues: BMBL: X06700; NID: 930053; PIDN: CAA29886.1; PID: 930054
A; Cross-references: EMBL: X06700; NID: 930053; PIDN: CAA29886.1; PID: 930054
B; Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A; Title: Covalent structure of collagen: amino acid sequence of alphal (I
A; Recence number: A90446; MUID: 81208139; PMID: 7016180
A; Molecule type: protein
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A,Cross-references: GDB:118729; OMIM:120180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
:Residues: 1065-1155,'P',1157-1466 <LOI>
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A;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
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                                                                                                                                                                                                                                                                                   Status: translation not shown
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A, Molecule type: mR
A, Residues: 1065-11
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951 GITGARGLAGPPGMPGPRGSPGPQGVKGESGKPGANGLSGERGPPGPQGLPGLAGTAGEP 1010
                                                                                                                                                                                                                                 294 GAPGPMGPRGAPGERGRP---GLPGAAGARGNDGARGSDGQPGPPGTPGTPGFPGSPGAK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GPPGPPGARGQAGVMGFPGPK---GAAGEPGKAGERGVPGPPGAVGPA---GKDGEA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 GEVGPAGSFGSNGAPGQRGEPGPQGHAGAQGPPGPPGINGSPGGKGEMGPAGIDGAPGLM 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 GEPGANGLPGAAGERGAPGFRGPAGPNGIPGEKGPAGERGAPGPAGPRGAAGEPGRDGVP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GAQGPPGPAGPAGERGEQGPAGSPGFQCLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 GARGPPGPAGANGAPGLRGGAGEPGKNGAKGEPGPRGERGEAGIPGVPGAKGEDGKNGSP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPGAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 GKNGERGGPGGPGPPGKNGETGPQGPPGPTGPGGDKGDTGPPGPQGLQGLPGTGGPP 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------GPSGPAGEPGPT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       651 GENGKPGEPGPKGDAGAPGARGKGDAGAPGERGPPGLAGAPGLRGGAGPPGPEGGKGAA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 GLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSP-------GPAGPKGSP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               463 GEAGRP---GEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQAGV- 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       771 GPAGQPGDKGEGGAPGLPGIAGPRGSPGERGETGPPGPAGFPGAPGQNGEPGGKGERGAP 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 GPTGL-----PGPPGERGGPGSRGF-----PGADGVAGPKGPAGERGSPGPKGSP 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 GPPGPPGAAGTPGLQCMPGERGGLGSPGPKGDKGEPGGPGADGVPGKDGPRGPTGPLGPP 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --MGFPGPKGAAGEPGKAGERGVPGP--------PGAVGPAGKDGEAGAQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        831 GEKGEGGPPGVÁGPPGGSGPAGPPGPGGVKGERGSPGGPGAAGFPGÁRGLPGPPGSNGNP 890
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                                                                                                                                                                                                                                                                                                                                           GSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRP-----
; Score 2370; DB 1; Length 1466;
; Pred. No. 4.9e-111;
56; Mismatches 285; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 GEAGKPGEOGVPGDLGAP-------
                                                                                                                                                                          1 GPPGEPGPTGLPGPPGERGGPGSRGFP-----
                                    49.5%;
                                         Best Local Similarity 49.59
Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \stackrel{>}{\circ}
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Filo64-1066/Region: cell attachment (R-G-D) motif
Filo64-1066/Region: cell attachment (R-G-D) motif
Filo64-1066/Region: cell attachment (R-G-D) motif
Filo67-1069/Region: cell attachment (R-G-D) motif
Filo7-1099/Region: cell attachment (R-G-D) motif
Filo87-1039/Region: cell attachment (R-G-D) motif
Filo87-1036/Region: cell attachment (R-G-D) motif
Filo87-1136/Region: cell attachment (R-G-D) motif
Filo87-1496/Domain: carboxyl-terminal homology cFCC>
Filo87-1496/Domain: fibrillar collagen carboxyl-terminal mature form) #status predicted
Filo87-1936-608.614.1004.1007.1013.1028.1034/Modified site: 4-hydroxylysine (Lys) #status predicted
Filo89/1339/Binding site: carbohydrate (Lys) #status predicted
Filo89/1329/Dishilfide bonds: interchain #status predicted
Filo89.1329/1325/Dishilfide bonds: interchain #status predicted
Filo89.1329.1327/Dishilfide bonds: #status predicted
                                                                                                                                                                                                         type V procollagen COOH-termina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: DNA
A; Residues: 1449-1465, 'A' <TSI>A; Residues: 1449-1465, 'E', 1465-1495, 'A' <TSI>A; Residues: 1491-1465, 'E', 1465-1495, 'A' <TSI>A; Cross-references: GB: 030551, NID: 9179695, PIDN: AAA51858.1; PID: 9179696
A; Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for residu C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (are 5-hydroxylated and subsequently O-glycosylated.
C; Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119064; CMIM:120190
A;Map position: 2q31-2q31
A;Introns: 33/1; 812/3; 830/3; 848/3; 894/3; 902/3; 974/3; 1046/3; 1064/3; 1448/3
CComplex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), a alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: structural component of extracellular fibrous polymer associated with cell A; Note: may play a role in controlling the lateral growth of collagen I fibrils A; Note: may play a role and controlling the lateral growth of collagen I fibrils C; Superfamily: collade alpha alpha in; fibrilar collagen carboxyl-terminal homology; C; Keywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproll; F; 1-26/Domain: signal sequence #status predicted <a href="Missangle-Right-Argorithm-1">Missangle-Right-Argorithm-1</a>; P; 27-1250/Product: collagen alpha 2(V) chain #status predicted <a href="Missangle-Right-Argorithm-1">Missangle-Right-Argorithm-1</a>; P; 27-1050/Product: collagen alpha 2(V) chain #status predicted <a href="Missangle-Right-Argorithm-1">Missangle-Right-Argorithm-1</a>; P; 27-1050/Product: colladand factor type C repeat homology <a href="Wissangle-Right-Argorithm-1">WCS</a>; P; 109-1265/Region: collattachment (R-G-D) motif</a>; P; 203-1265/Region: cell attachment (R-G-D) motif</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COL3A1 and COL5A2, located
                                                                                                                                                                                                                                                                                                                          A Molecule type: mRNA
A Mesidues: 1227-1417, T',1419-1437,'S',1439-1496 <MYE>
A) Residues: 1227-1417, T', 1419-1437,'S',1439-1496 <MYE>
A) Experimental source: normal fibroblasts
A) Experimental source: normal fibroblasts
Gristpouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, A; Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, A; Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, locat A; Reference number: A30017; MUID: 89138450; PMID: 3224983
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              A,Cross-references: GB:MI1135, NID:g179693; PIDN:AAA51857.1; PID:g179694 A,Note: part of this sequence were determined by protein sequencing F,Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
J. Loidl, H.R.; Seyer, J.M.; Dion, A.S.
J. Biol. Chem. 260, 11216-11222, 1985
A,Title: Complete primary structure of the human alpha-2 type V procollace. A,Reference number: A25374; MUID:85289337; PMID:2411731
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48.2%; Pred. No. 7.6e-109;
ive 52; Mismatches 287;
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Matches 478;
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A;Molecule type: mRNA
A;Residues: 1003-1034 <RES>
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GPPGEPGDPGPMGPIGSRGPEGPPGKPGEDGEPGRNGNPGEVGFAGSPGARGFPGAPGLP 296
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49607
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R;Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
Dev. Dyn. 195, 113-120, 1992
A;Title: Localization of pro-alpha 2(V) collagen transcripts in the tissues of the deve A;Reference number: 149607; MUID:93214071; PMID:1297453
A;Accession: 149607
A;Accession: 149607
A;Accession: 149607
A;Residues: 1-1497 ARES
A;Cross-references: UNIPROT:Q61431; GB:L02918; NID:g309180; PIDN:AAA37440.1; PID:g30918
A;Gross-references: UNIPROT:Q61431; GB:L02918; NID:g309180; AWA37440.1; PID:g30918
C;Genetics:
A;Gene: Collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
F;39-98/Domain: von Willebrand factor type C repeat homology <VWC>
F;1270-1497/Domain: fibrillar collagen carboxyl-terminal homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLKGHRGHKGLEGPKGEIGAPGAKGEAGPTGPMGAMGPLGPRGMPGERGKLGPQGAPGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GPPGAVGPAGKDGBAGAQGP---PGPAGPAGERGEQGPAGSPGFQGLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 GPPGEPGEPGPMGPIGSRGPEGPPGKPGEDGEPGRNGNTGEVGFSGSPGARGFPGAPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPGEAGKPGEOGVPGDLGAPGPS---GPAGEPGPTGLPGPPGERGGPGSRGFPGADGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 --AGEPGPTGLPGPPGBRGG------PGSRGFPGADGVAGPKGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPPGEP-----GPTGLPGPPGE------RGGPGSRGFPGADGVA
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Local Similarity 47.6%; Pred. No. 9.9e-108; Longth 1497;
Local Similarity 47.6%; Pred. No. 9.9e-108;
Local Similarity 47.6%; Mismatches 289; Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGP
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| 277 GSPGSPGPDGKTGPPGPAGODGRPGPPGARGQAGWMGFPGPKGAAGEPGKAGERGVP 3 460 GSPGIN  | 05   040 GASGPGGLPGGRGAGGRGETGLRGDTGNTGRDGARGIPGAVGAPGFAGASGGDR 699     07   08   08   08   08   08   08   08  | Qy         595 GKPGEQGVPGDLGAPGPSGPAGEFGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPA 651           Db         874 GAPGILGIPGSRGERGLPGIAGALGEPGPLGISGPPGARGPPGANGSPGVNGAPGEA 930           Qy         652 GERGSPGPAGPKGSPGBAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPP 711           Db         931 GRDGNPGSDGPPGRDGPGRGRGRGRGPGSRGPGPGKGGRGRGPRGPP 990           Qy         712GPPGARGQAGVMGFPGRKGAAGEPGKAGBRGVPGPPGAVGPAGKDGEAGAQ 762           Db         991 GSVGPVGAVGFRGPGGPGRGEPGKKGERGUPGPPGAVGPAGKDGEAAAQ 762           Db         991 GSVGPVGAVGFRGPSGPGGRRGEPGKKGERGLPGLKGYSGLQGLHGDQGAP 1050   | Oy 763 GPPGPAGPAGERGEOGPAGSPGFGGLPGPAGPPGEDGEVPGDLGAPGPSGPAG 820   |  |                  |   |
|---|--|---|--|--|------------------|---|
| Db 1012 GTPGKVGPTGATGDKGPPGPGSNGPVGEPGPAGNDGTPGRDGAVGERGDRGDP 1071  Qy 700 GPAGQDGRPGPPGARGAGWGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKD 756 | RESULT 15 A43291 colladen alpha 2(I) chain precursor - mouse colladen alpha 2(I) chain precursor - mouse colladen alpha 2(I) chain precursor - mouse c;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A42291; A54328 R;Phillipps, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J. Genomics 13, 1345-1346, 1992 A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2(I) collagen A;Reference number: A43291; MUID:92372043; PMID:1505972 A;Status: preliminary; not compared with conceptual translation | A; Molecule Lype: mRNA A; Residues: 1-1373 (PHI> A; Cross-references: UNIPROT:Q01149; GB:X58251; NID:g50488; PIDN:CAA41205.1; PID:g50489 A; Cross-references: UNIPROT:Q01149; GB:X58251; NID:g50488; PIDN:CAA41205.1; PID:g50489 A; Note: sequence extracted from NCBI backbone (NCBIP:112027) B; Phillibs, C.L.; Lever. L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J. J; Invest. Dermatol. 97, 980-994, 1991 A; Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polymera A; Accession: A54328; MUID:92084969; PMID:1748823 A; Accession: A54328 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA C; Genetics: 1-110 < PHZ> C; Genetics: | A, Gener COLIA2  C, Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology C; Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology (FCC; E; 1145-137) Domain: fibrillar collagen carboxyl-terminal homology (FCC)  Query Match  Query Match  Query Match  A 9.6%; Score 2300; DB 1; Length 1373;  Best Local Similarity 47.4%; Pred. No. 1.46-107;  Matches 483; Conservative 50; Mismatches 275; Indels 210; Gaps 20; | QY         1 GPPGEPGPTGLPGPPGRGGPGSRGPPGADGVAGPKGPPGBRGSPCBAGPKGSPGBAGRP 60           Db         103 GPRGPPGAVGAPGPGPGSPGBPGQTGPAGPRGPAGSPGKAGBDGHPGKPGRP 159           QY         61 GEAGLPGAKGLTGSPGSPGPDGKTGPPGPBAGQDGRPGPPGARGQA 108           I | PGPPGAVGPAGKDGEA | Db 340 GAAGATGARGLVGEPGPAGSKGESGNKGEPGSVGAQGPPGPSGEEGKRGSPGEAGSAGPA 399  Qy 217 GPPGERGFPGADGVAGPKGPAGERGSPGFAGPKGSPGEAGRPGEAGLPGAKGLT 276  Db 400 GPPGLRGSPGSRGLPGANGRPGNRGSPGRRGSPGRPGEPGLMGPRGLT 1 |

October 18, 2004, 13:23:10 ; Search time 146.729 Seconds (without alignments) 3219.411 Million cell updates/sec US-10-658-989A-3 4640 1 GPPGEPGPTGLPGPPGERGG......GEQGVPGDLGAPGPSGPAGG 821 1825181 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 1825181 segs, 575374646 residues OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database :

## SUMMARIES

|           |                |            |        |            |            |                 |            |                    |                    |          |            |                    |                    |                    |                    |          |        |        |        |        |        |            |        |        |        |        |            |        |        |        |        | _                  |
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|           | Description    | homo.      | OMOU.  | m          | cani       |                 |            | 081019 mus musculu | Q6lan8 homo sapien |          |            | 093251 rana catesb | Q9yib4 cynops pyrr | Q802b5 xenopus lae | Q6pcl3 mus musculu |          |        |        |        |        |        |            | gallus | gall   | mus    | mus    | mus        | mus    | _      | m      | _      | Q6p4ul brachydanio |
| SUMMARIES | ID             | CA11_HUMAN | 076045 | Q8N473     | CA11_CANFA | Q630 <u>7</u> 9 | CA11 MOUSE | Q810 <u>J</u> 9    | Q6LAN8             | CAA67261 | CA11_CHICK | 093251             | Q9YIB4             | Q802B5             | Q6PCL3             | AAH59281 | 014046 | Q14047 | 077753 | Q91B91 | Q28396 | CA12 HUMAN | Q90W37 | Q7T2Z7 | Q62031 | 062033 | CA12_MOUSE | Q62032 | QBOVY3 | Q63123 | Q80X38 | Q6P4U1             |
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| d         | Query<br>Match | 9          | 59.5   | 59.5       | 59.5       | 59.2            | 58.9       | 58.9               | 57.8               | 57.8     | 57.7       |                    |                    |                    |                    |          |        |        |        | 53.4   | 53.4   |            |        |        | S      | 53.1   | Ŋ          | 53.    | ß      | S      | 52.8   | 52.4               |
|           | Score          | 2765       | 2761   | 2761       | 2759       | 2748.5          | 2732.5     | 2732.5             | 2681.5             | 2681.5   | 2679       | 2568               | 2561.5             | 2529               | 2494               | 2494     | 2486   | 2486   | 2481   | 2479   | 2477   | 2476       | 2475.5 | 2465.5 | 2464   | 2464   | 2464       | 2464   | 2455   | 2454   | 2449   | 43                 |
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| Aah63249 brachydan | Q6ulj5 brachydanio | Aar24536 brachydan | Q9w7r9 cynops pyrr | Q6p4z2 xenopus tro | Aah63191 xenopus t | Q91717 xenopus lae | Q7zti6 xenopus lae | Q6pei9 brachydanio | Aah58045 brachydan | Q91718 xenopus lae | Q7ztm4 xenopus lae | Q6nz15 brachydanio | Aah66384 brachydan |  |
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| AAH63249           | Q6U1J5             | AAR24536           | Q9W7R9             | O6P4Z2             | AAH63191           | 091717             | O7ZTI6             | O6PEI9             | AAH58045           | 991718             | O7ZTM4             | O6NZ15             | AAH66384           |  |
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| 52.4               | 52.3               | 52.3               | 52.0               | 51.8               | 51.8               | 51.7               | 51.7               | 51.5               | 51.5               | 51.4               | 51.4               | 51.4               | 51.4               |  |
| 2430               | 2428.5             | 2428.5             | 2412               | 2405               | 2405               | 2401               | 2399               | 2390               | 2390               | 2386               | 2385               | 2384               | 2384               |  |
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## ALIGNMENTS

| RN DICCINCTURE OF ACT 1464 DECM N N |
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                                                                                                                                                                                              SEQUENCE OF 175-187 AND 274-289.
PubMed=2169412;
                                                                                               SEQUENCE OF 1229-1454 FROM N.A.
                      SEQUENCE OF 472-607 FROM N.A.
                                            488-625 FROM N.A.
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                                            SEQUENCE OF 488
PubMed=3857621;
                                                                                                                                                                                                                           TISSUE=Skin;
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1139 GPRGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGPVGPPGPPGPPG

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REVIEW ON OI VARIANTS. MEDLINE=91374476; PubMed=1895312;

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SEQUENCE FROM N.A.
MEDLINE=98107942; Pubmed=
Korkko J., Ala-Kokko L.,
Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matrix 11:375-379(1991).
                                PRELIMINARY;
                                                                                                                                              Homo sapiens (Human)
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Mammalia; Eutheria;
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Length 1464;
 Score 2765; DB.1;
Pred. No. 2.6e-103;
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                  ; Pred. No. 2.6e
31; Mismatches
 59.6%;
                                Matches 561; Conservative
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MEDIINE=89025644; PubMed=3178743; Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T., Jaenisch R., Prockop D.J.; Structure of a full-length cDNA clone for the prepro alpha 1(I) chain of human type I procollagen."; Biochem. J. 253:919-922(1998).
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GO, GO:0005581; C:collagen; IEA.

GO, GO:0005737; C:cytoplasm; IEA.

GO, GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0006817; P:phosphate transport; IEA.
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Am. J. Hum. Genet. 62:98-110(1998).
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MEDLINE=85130970; PubMed=2857713;
Chu M.L., de Wet W., Bernard M., Ramirez F.;
"Fine structural analysis of the human pro-alpha 1 (1) collagen Promoter structure, Alul repeats, and polymorphic transcripts.";
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MEDLINE=92157916; PubMed=1787829;
Westerhausen A., Constantinou C.D., Pack M., Peng M.Z., Hanning Olsen A.S., Prockop D.J.;
"Completion of the last half of the structure of the human gene the Pro alpha I (I) chain of type I procollagen (COLIAI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=88329734; PubMed=2843432;
D'Alessio M., Bernard M., Pretorius P.J., de Wet W., Ramirez F. "Complete nucleotide sequence of the region encompassing the fiventry-five exons of the human pro alpha 1(1) collagen gene."; Gene 67:105-115(1988).
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tko i., De Paepe A., Nuytinck i., Barley J.,
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Primates, Catarrhini, Hominidae,
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Last sequence update)
Last annotation update)
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Highly conserved sequences in the 3-untranslated
COLIA1 gene bind cell-specific nuclear proteins.";
FBSS Lett. 279:9-13(1991).
                                                                     PRT;
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                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26, Pro alpha 1(1) collagen.
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GKAGERGVPGPPGAVGPAGKDGE-------AGAQGPPGP-
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 25, Last annotation update)
Alpha I type I collagen, preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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llarity 55.3%; Pred. No. 3.8e-103;
Conservative 31; Mismatches 229;
                                          Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18
Probom; P000207; Cighelix; 3.
Probom; P0002078; Fib_collagen_C; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS501208; VWFC 1; 1.
PROSITE; PS50184; VWFC 1; 1.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
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R G0; G0:0005591; C:collagen; IEA.

G0; G0:0005201; C:collagen; IEA.

R G0; G0:0005201; F:extracellular matrix structural constituent; IEA.

R G0; G0:0005201; F:extracellular matrix structural constituent; IEA.

R G0; G0:0005201; P:extracellular matrix structural constituent; IEA.

R InterPro; IPR008161; Cig_helix.

R InterPro; IPR008161; Collagen.

R InterPro; IPR001009; WPP_GGI.

R Pfam; PF01410; CoLFF; 1.

R Pfam; PF01410; CoLFF; 1.

R Pfam; PF01410; CoLFF; 1.

R ProDom; PD000007; Cig_helix; 3.

R ProDom; PD000078; Fib_collagen_C; 1.

SMART; SM00214; VWC; 1.
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                                                                                                                  GLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEP
                                                                                                                                                                                                                  GAEGSPGRDGSPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKSGDRGETGPAGPV
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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TISSUBErain;
Strausberg R.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                          GDKGESGPSGPAGPTGARGAPGDRGEPGPPGPAGPAGPPGADGQPGAKGEPGDAGAKGDA
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                                                                                                        GPMGPSGPRGLPGPPGAPGPQGPQGPPGEPGASGPMGPRGPPGPPGKNGDDGEAGKP
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                                                                                       1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEA---
                                                                    Gaps
                                                                   Indels 192;
                                              Length 1464;
                            1464 AA; 139010 MW; B0581F8D1C89DDE8 CRC64;
                                               Score 2761; DB 2;
Pred. No. 3.8e-103;
1; Mismatches 229;
                                                                                                                              GRPGEAGLP---GAKGLTGSPGSPGP-----
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                                                                   31;
                                               Query Match
Best Local Similarity 55.3%;
Matches 560; Conservative 3:
PS501208; VWFC 1; 1. PS50184; VWFC 2; 1.
                    Collagen.
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstands. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campbell B.G., Wootton J.A.M., MacLecd J.N., Minor R.R.; "Sequence of normal canine COLIA1 cDNA and identification of a heterozygous alphal(I) collagen Gly208Ala mutation in a severe case of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canine osteogenesis imperfecta.";
Arch. Blochem. Blophys. 384:37-46(2000).
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- PTM: Profiles at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- DISEASE: Defects in COLIA1 are a cause of osteogenesis imperfecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disease mutation; Extracellular matrix;
Pyrrolidone carboxylic acid; Repeat;
                                                                                                                                                                                                                         30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(1) chain precursor.
Name=COLIA1;
Canis familiaris (Dog).
Eukaryota; Mecazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                       1139 GPRGPPGSAGAPGKDGLNGLPGPPGPPGRTGDAGPVGPPGPPGPPGPPG
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Triple-helical region.
Nonhelical region (C-terminal).
Cell attachment site (Potential)
Cell attachment site (Potential)
Pyrrolidone carboxylic acid (By
GERGEOGPAGSP---GFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAG
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Allysine (By similarity).
5-hydroxylysine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the fibrillar collagen family. -!- SIMILARITY: Contains 1 VWFC domain.
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Collagen alpha 1(I) chain.
C-terminal propeptide.
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TISSUE=Skin;
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InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR00160; Collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01391; Collegen; 18.
ProDom; PD002079; Fib_collagen_C; 1.
ProDom; PD002079; Fib_collagen_C; 1.
PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01208; VWFC_2; 1.
Collagen; Connective tissue; Disease much proproceden; Pydroxylation; Pyrrolidor
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(TrEMBLrel. 01, (TrEMBLrel. 06, 1 (TrEMBLrel. 26, 1
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                                                                                                      PRELIMINARY;
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Matches 556; Conserv
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                487 GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD
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50 3-hydroxyproline (By similarity).
51 0-linked (Gal. .) (By similarity).
51 N-linked (GloNAc. .) (By similarity).
63 G -> A (in OI; severe).
64 138762 MW; 58E3674D2B570697 CRC64;
                                                                                                    Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQ--------
                                                                            Length 1460;
                                                                          Score 2759; DB 1;
Pred. No. 4.5e-103;
                                                                                                    31; Mismatches 230;
                                                                                                                                                                                                                                                                                                                                        GPSGPA----
                                                                                                                                                                                                                                                                                                                                        GVPGDLGAP------
                                                                            59.5%;
                                                                                                      Conservative
              261
1361
                                      208
                                      208 20
1460 AA;
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPSGPAGE-
                                                                                        Best Local Simi
Matches 559;
 MOD RES
CARBOHYD
CARBOHYD
                                      VARIANT
SEQUENCE
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---GPSGPA-----GEPGPTGLPGPPGER 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley, TISSUE=Bone, and Tooth;
MEDINE=9915824; PubMed=10065941;
Brandsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
"Expression of collagen alphal(I) mRNA variants during tooth and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 GPPGQDGIPGQPGLPGPPGPPGPLGLGGNFASQMSYGYDEKSAGVSVPGPMGPSGPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 GERGRPGPPGTAGARGNDGAVGAAGPPGPTGPPGFPGAAGAKGEAGPQGARGSEGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 GERGVPGPPGAVGPAGKDGEAGAQGPPGP------AGPAGERGEQGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --AGSPGFQGLPGPAGPPGEAGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 GVRGEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQGPSGAP
                                                                                                                                                                                                                                                                                                                                                                                                     Collagen alphal (Fragment).
Rattus norvegicus (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0005581, C:collagen, IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR008161; Cig_helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00865; Fib_collagen_C.
InterPro; IPR009041; PMP-SGCI.
InterPro; IPR001007; VMP-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GPKGAAGEPGK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243;
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                                       1147 GKDGLNGLPGPPGPPGRRTGDAGPVGPPGPPGPPG 1186
   820
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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larity 52.3%; Pred. No. 1.2e-102;
Conservative 33; Mismatches 231;
---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPPGE---PGPTGLPGPPGERGGPGSRGFPG-----
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Prodom; PD002078; Fib_collagen_C; 1.
SMART; SM0038; COLFT; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             formation in the rat.";
J. Dent. Res. 78:11-19(1999).
EMBL; Z78279; CAB01633.1; -.
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19;

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236

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collagen

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESQUENCE OF 1442-1453 FROM N.A.

WEDLINE-88124276, PubMed=3340560;
Mooslehner K., Harbers K.;
Mooslehner K., Harbers K.;
Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size of RT Two mRNAs of mouse pro alpha 1(I) collagen is a member of group I collagen

CC (fibrillar forming collagen):
CC (fibrillar forming collagen)
CC (1: SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
CC -: TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium

Nutrinavanatite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- SIMILARITY: Belongs to the fibrillar collagen family.
-!- SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                procellagen gene:
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 735-878 AND 1005-1058 FROM N.A. MEDLINE-83157109; PubMed-6219867; Monson J.M., McCarthy B.J., Midentification of a Balb/c mouse pro alpha 1(I) procollagen gene: evidence for insertions or deletions in gene coding sequences."; DNA 1:59-69(1981).
                                                                                              pro alpha 1(I)
                                                                                                                                                                                                                              MEDLINE=83141374; PubMed=6298597; McCarthy B.J.; Mc
                                                                                                 for mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, SS7243, S11626.

MGD, MGI:88467, Collal.

InterPro; IPR008161, Collagen.

InterPro; IPR008165, Collagen.

InterPro; IPR009041; PMP_SGCI.

InterPro; IPR009041; PMP_SGCI.

InterPro; IPR009041; VMP_C.

Pfam; PF01410; CoLFI; 1.

ProDom; PD000007; CIg hellx; 1.

ProDom; PD0000078; Fib_collagen_C; 1.

SMART; SM00214; VWC; 1.
                      SEQUENCE OF 518-1128 FROM N.A. MEDLINE-86137403; WENDARD 3841523; French B.T., Lee W.-H., Maul G.G.; "Nucleotide sequence of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U08020) AAA88912.1;

EMBL, X15896, CAA33904.1;

EMBL, M1442; AAA3333.1;

EMBL, X06753, CAA29927.1;

EMBL, K03026, AAA37332.1;

EMBL, K03030, AAA37332.1;

EMBL, K03030, AAA37332.1;

EMBL, K03031, AAA37332.1;

EMBL, K03031, AAA37332.1;

EMBL, K03033, AAA37332.1;

EMBL, K03034, AAA37332.1;

EMBL, K03035, AAA37332.1;
                                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 2:1362-1371(1982)
                                                                                                                                                                                                        SEQUENCE OF 735-1130 FROM N.A.
                                                                                                                                                   Gene 39:311-312(1985).
1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1017 GAPGAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKNGDRGETGPAGPAGPIGPAGARGPA 1076
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282
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                                                                                                                                                                                                                                                                                                                    GAPGPSGARGERGFPGERGVQGPPGPAGPRGNNGAPGNDGAKGDTGAPGAPGSQGAPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFPGADGVAGPKGPAGERGSPGPAGPKGSPGE-----AGRPGEAGLPGAK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     897 GPRGETGPÁGRPGEVGPPGPPGPAGEKGSPGADGPAGSPGTPGPQGIAGQRGVVGLPGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 GERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAKGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1077 GPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGEGGPSGASGPAGPRGPPGSA
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                                                                                                            GGPGSRGFPGADGVAGPKGPSGERGSPGPAGPKGSPGBAGRPGEAGLPGAKGLTGSPGSP
                                                                                                                                                                                  GPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAV
                                                                                                                                                                                                                                 537 GPDGKTGPPGPAGQDGRPGPAGPPGARGQAGVMGFPGPKGTAGEPGKAGERGVPGPPGAV
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                                                                                                                                                                                                                                                                                      GPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1137 GSPGKDGLNGLPGPPGPRGRTGDSGPAGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 GSP---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG 820
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Li S.W., Khillan J., Prockop D.J.;
"The complete cDNA coding sequence for the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA11_MOUSE STANDARD; PRT; 1453 AA. P11087; Q66635; C1-UUL-1999 (Rel. 11, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) collagen alpha 1(1) chain precursor. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of type I procollagen.";
Matrix Biol. 14:593-595(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745
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CAll_MOUSE
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(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequ
(TrEMBLrel. 26, Last anno
                                                                                                                                                                                                                                                                                                                           Procollagen, type I, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
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01-JUN-2003 (
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                     Name=Collal;
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                     840
                                                                                                                      688
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 523
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Q810J9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486
                                                                                                                                                                                                                                                                                                                180 GPPGAPGPQGFQGPPGEPGEPGSGPMGPRGPPGFNGDDGEAGKPGRPGERGPPGPQ 239
                                                                                                                                                                                                                                                                                                                                                       240 GARGLPGTAĞLPGMKGHRGFSGLDGAKGDAĞPAĞPKĞEPĞSPĞBNĞAPĞQMĞPRĞLPĞER 299
                                                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                                         300 GRPGPPGTAGARGNDGAVGAAGPPGPTGPPGFPGAVGAKGEAGPQGARGSEGPQGVR 359
                                                                                                                                                                                                                                                                                                                                                                                                                   GAQGPPGPAGPAGERGEQGP-------AGSPGFQGLPGPAGPPGEAGKPGEQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                       GEPGPPGPAGAAGPAGNPGADGQPGAKGANGAPGIAGAPGFPGARGPSGPQGPSGPPGPK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVPGDLGAP-----GPSGPA-----GPSGPA-----GRPGPTGLPGPPGERGGP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSRGFPGADGVAGPKGPSGERGAPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPD 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGLPGPPGERGGPGSRGFP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERGAAGLPGPKGDRGDAGPKGADGSPGKDGARGLTGPIGPPGPAGAPGDKGEAGPSGPP 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPSGARGERGFPGERGVQGPPGPAGPRGNNGAPGNDGAKGDTGAPGAPGSQGAPGLQGMP 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPD-----GKTGPPGPAGQDGRPGPPGPPGARGQ------AGVMGFP 522
                                                                                                                                                                                                                                                                                              -----RGGPGSRGFPGADGVAGPKGPAGERGSPGPA 48
                                                                                                                                                                                                                                                                                                                                    GPKGSPGEAGRP------GEAGLPGAKGLTGSPGSPGFDGKTGPPGPAGQD 93
                                                                                                                                   Allysine (By similarity).
5-hydroxylysine (By similarity).
3-hydroxyproline (By similarity).
N-linked (GlcNac.). (Potential).
O-linked (GlcNac..) (By similarity).
N-linked (GlcNac..) (By similarity).
Cell attachment site (Potential).
A -> V (in Ref. 5).
                                                                                                                                                                                                                                                                                                                                                                            GRPGPPGPPGARGQAGVMGFPGPKGAAGE-----PGKAGERGVPGPPGAVGPAGKDGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADGVAGPKGPAGERGSPGPAGPKGSPGB-----AGRPGEAGLPGAKGLTGSPGSP
                                                                                                                                                                                                                                                                          Gaps
                    e, Extracellular matrix, Glycoprotein, carboxylic acid, Repeat, Signal.
                                                                                                                                                                                                                                                      DB 1; Length 1453;
                                                                                                                                                                                                                                                                         33; Mismatches 240; Indels 180;
                                                                                        Nonhelical region (N-terminal).
Triple-helical region.
Nonhelical region (C-terminal).
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                   3B802E535DF81808 CRC64;
                                                  N-terminal propeptide.
Collagen alpha 1(I) chain.
                                                                     C-terminal propeptide.
                                                                                                                                                                                                                                                    Score 2732.5; DB 1
Pred. No. 5.2e-102;
                                                                                                                                 similarity)
                                                                                                                                                                                                                                   137944 MW;
PROSITE, PS01208; WWFC_1; 1.
PROSITE, PS50184; WWFC_2; 1.
Collagen; Connective tissue;
Hydroxylation; Pyrrolidone ca
                                                                                                                                                                                                                                                     58.9%;
                                                                                                                                                                                                                                                                                             1 GPPGEPGPTGLPGPPGE
                                                                                                                                                                                                                                                                Best Local Similarity 54,7
Matches 547; Conservative
                                                  151
1207
1453
1453
167
167
1181
1207
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254
1153
56
254
1354
736
1084
1450
                                                                                                                                                                                                                                   AA;
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1450
1453
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MOD_RES
MOD_RES
CARBOHYD
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                                                                                                                                                                                                              SITE
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                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                      MOD_RES
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DOMAIN
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STAIN=FVBN/N; TISSUE—Colon;
STAIN=FVBN/N; TISSUE—Colon;
STAIN=FVBN/N; TISSUE—Colon;
MEDLINE—22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Distchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunerane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villadon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs X.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodiigues S., Sanchez A.,
Bukelley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blacelley R.W., Touchman J.W., Green B.D., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                       630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           746
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570
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GPKGAAGEPGKAGERGVPGPPGA------VGPAGKDGEAGAQGPPGPAGP--AGER
                                                                                                                                                                                                                                                                                                                                                                                                                                            960 GFPGLPGPSGEPGKQGPSGSSGERGPPGPMGPPGLAGPPGESGREGSPGAEGSPGRDGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1080 GPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGBGGPSGASGPAGPRGPPGSAGSP
                                                                               GPIGNVGAPGPKGPRGAAGPPGATGFPGAAGRVGPPGPSGNAGPPGPPGPVGKEGGKGPR
                                                                                                                                                                            GEOGPAGSPGFOGLPGPAGPPGEAGKPGEOGVPGDLGAPGPSGPAGEPGPTGLPGPPGER
                                                                                                                                                                                                                                                           900 GETGPAGRPGEVGPPGPPGPAGEKGSPGADGPAGSPGTPGPQGIAGQRGVVGLPGQRGRGR
                                                                                                                                                                                                                                                                                                                                               GGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAKGLTGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC050014; AAH50014.1; -. MGD, MGI:88467; Collal. MGD, MGI:88467; Collal. GO; GO:0005581; C:collagen; IEA. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0005201; F:extracellular matrix structural constituent; IEA. GO; GO:0006817; P:extracellular matrix structural constituent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1140 GKDGLNGLPGPIGPPGPRGRIGDSGPAGPPGPPGPPG 1179
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Last annotation update)
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Æ
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.080 GPRGDKGETGEQGDRGIKGHRGFSGLQGPPGSPGSPGEQGPSGASGPAGPRGPPGSAGSP 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĠNDĠATĠAAĠPPĠPTĠPAĠPPGFPGAVĠAKĠĒĀĠPQĠPRĠSEĠPQĠVŔĠĒPĠPGPAGAA 382
                                                                                                                                 1020 GAKGDRGETGPAGPPGAPGAPGAPGPVGPAGKNGDRGETGPAGPAGPIGPAGARGPAGPO
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                                                                                                                                                                                     1 GPPGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRP
  GGPGSRGFPGADGVAGPKGPAGERGSPGPAGP---KGSPGEAGRPGEAGLPGAKGLTGSP
                                                                                               688 GSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDINE-97141927; PubMed=8988177; Sirvent N., Kedra D., Guilbaud C Simon M., Pedeutour F., O'Brien K., Sirvent N., Kedra D., Guilbaud C Turc-Carel C., Dumanski J.P., "Regulation of the platelet-derived growth factor B-chain gene via fusion with rollagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma."; Nat. Genet. 15:95-98(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L SUBLICH K.P.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; X99705, 12467261.1;

InterPro: IPRO0161; Clg helix.

R InterPro: IPRO0160; Collagen.

R InterPro: IPRO01941; PWP_C.

R InterPro: IPRO01007; VWP_C.

R Pfan; PPO1391; Collagen; 15.

R Pfan; PPO10391; VWC; 1.

R ProDom; PD000007; Clg helix; 3.

R RARRI; SM00214; VWC; 1.

R PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97445 MW; EE279B10572FB980 CRC64;
                                                                                                                                                                                                                                                                                                          1140 GKDGLNGLPGPIGPPGPRGRTGDSGPAGPPGPPGPPG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGLAN8;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Collagen type I alpha I (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                  784 ---GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%; Score 2681.5; DB 2; 58.4%; Pred. No. 4.6e-100; iive 28; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.49
Matches 524, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069
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1069 A.A.;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
       631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                COCCEPTOR SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Collagen.
InterPro; IPR009081; Pib_collagen_C.
InterPro; IPR001007; VWF_C.
Ffam; PF01410; Collagen; 18.
Pfam; PF01391; Collagen; 18.
Pfam; PF001991; Collagen; 18.
ProDom; PD000007; Clg_helix; 3.
ProDom; PD000070; Clg_helix; 3.
ProDom; P000180; VWC; 1.
SWART; SW00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
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Matches 547; Conservative
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Turc-Carel C., Dumanski J.P.;

Turc-Carel C., Dumanski J.P.;

Turc-Carel C., Dumanski J.P.;

Fregulation of the platelet-derived growth factor B-chain gene via fusion with collagen gene COLIA1 in dermatofibrosarcoma protuberans and giant-cell fibroblastoma.";

and giant-cell fibroblastoma.";

BMBL, X99705; CA567261.1;

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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Colladen type I alpha 1 (Fragment).
COLIA1.
COLIA1.
Bukaryeins (Hunan).
Bukaryeis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                        GPPGEPGEPGASGPMGPRGPPGPPGKNGDDGEAGKPGRPGERGPPGPQGARGLPGTAGLP
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                                                                                                                                                                                                   GMKGHRGFSGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLPGERGRPGAPGPAGAR
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                                                                117;
                                  2; Length 1069;
                                                                Indels
                              Query Match 57.8%; Score 2681.5; DB 2; Best Local Similarity 58.4%; Pred. No. 4.6e-100; Matches 524; Conservative 28; Mismatches 229;
EE279B10572FB980
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97446 MW;
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1069 AA;
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MEDLINE-72243016; PubMed=5047697;
Eyre D.R., Glincher M.J.;
"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";
Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=81160715; PubMed=6927845; Fuller F., Boedtker H.; "Sequence determination and analysis of the 3' region of chicken proalpha 1(I) and pro-alpha 2(I) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences."; Biochemistry 20:996-1006(1981).
                                                      Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                              MEDINE-82231995; PubMed-7093229;
Highberger J.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Kang A.H.
Gross J.;
                                                                                                                                                                                                                                                                                                                                                                       "Amino acid sequence of chick skin collagen alpha 1(I)-CB8 and the complete primary structure of the helical portion of the chick skin collagen alpha 1(I) chain."; Blochemistry 21:2048-2255(1982).
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MEDLINE=80134546; PubMed=6987088;

MEDLINE=80134546; PubMed=6987088;

MEDLINE=80134546; PubMed=6987088;

Pastan I., Descrombrugghe B., Fietzek P.P., Olsen B.R.;

"Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(1)-chains.";

FEBS Lett. 11:61-66(1980).

-!- FUNCTION: Type I collagen is a member of group I collagen

(fibrillar forming collagen).

-!- SUBMINT Trimers of one alpha 2(1) and two alpha 1(1) chains.

-!- SUBMINT Trimers of one alpha 2(1) and two alpha 1(1) chains.

-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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                                                                                                                                                                                                                                MEDLINE=88007542; PubMed=2820966;
Finer M.H., Aho S., Gerstenfeld D.C., Boedtker H., Doty P.;
Vinusual DNA sequences located within the promoter region and the
first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13322(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTW: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X. SIMILARITY: Belongs to the fibrillar collagen family. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                Finer M.H.; Boedtker H., Doty P.; "Construction and characterization of cDNA clones encoding the contracton pro alpha 1(I) collagen mRNA."; Gene 56:71.78(1987)
              Collagen alpha 1(I) chain precursor
                                                                                                                                    MEDLINE=88056316; PubMed=3678834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 981-1453 FROM N.A.
                                                                                                                       SEQUENCE OF 1-153 FROM N.A.
                                                                                                                                                                                                                      SEQUENCE OF 1-144 FROM N.A.
                                       Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 152-1187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxyapatite.
                                                                                              NCBI_TaxID=9031;
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GKDGEAGAQGPPGPAGPAGERGEQGP-----AGSPGFQGLPGPAGPPGEA 186
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5-hydroxyproline (Potential).
3-hydroxyproline.
0-linked (Gal. . .) (By similarity).
N-linked (GlCNAc. . .) (By similarity).
F -> L (in Ref. 5).
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30; Mismatches 250; Indels 186;
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7e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allysine (By similarity).
5-hydroxylysine (By similarity).
5-hydroxylysine (Potential).
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1441 1441 Q -> H (in Ref. 6).
1453 AA; 137789 MW; 3BC6152134271F4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         protein sequencing;
Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain.
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C-terminal propeptide.
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PROSITE; PS50184; VWFC_2; 1.
Collagen; Connective tissue; Direct protein
Extracellular matrix; Glycoprotein; Hydroxyl
Pyrrolidone carboxylic acid; Repeat; Signal
SIGNAL
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Probom, PD000007; Clg_helix; 2. Probom, PD002078; Fib_collagen_GSMART; SM0038; Col.Fi_1. SMART; SM00214; VWC; 1.
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X MEDLINE-92294154; Pubmed=10367734;

Asahina K., Utoh R., Obara M., Yoshizato K.;

Asahina K., Utoh R., Obara M., Yoshizato K.;

Asahina K., Utoh R., Obara M., Yoshizato K.;

T "Cell-type specific and thyroid hormone-dependent expression of genes

T of al (1) and a2(1) collagen in intestine duting

amphibianmetamorphosis.";

Matrix Biol. 1889-103(1999).

R Matrix Biol. 1889-103(1999).

R GO; GO:0005201; EAA390281; EAA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:000617; P:phosphate transport; IEA.

R InterPro; IPR0008160; Collagen.

R InterPro; IPR0008160; Collagen.

R InterPro; IPR000895; Fib collagen.

R InterPro; IPR000007; VWF_C.
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                                                GAVGPAGKDGEAGAQGPPGPAGPAGBRGEQGPAGSPGFOGLPGPAGPPGEAGKPGEOGVP 399
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534 GSPGPDGKTGPPGPAGQDGRPGPPGPRGARGQAGVMGFPGPKGAAGEPGKPGERGAPGPP 593
                                                                         594 GAVGAAGKDGEAGAQGPPGPTGPAGERGEQGPAGAPGFQGLPGPAGPPGEAGKPGEQGVP
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Namesalpha 1 type I collagen;
Rana catesbeiana (Bull Tordaca)
Eukaryota, Metazoa; Ghordaca; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKPGEQGVPGD--------LGAPGPSGP----
                                                                                                                                                                                                                               F59BB550C9873F04
                                                                                                                                                                                                                                                                            55.3%; Score 2568; DB 2; 153.6%; Pred. No. 1.9e-95; ive 43; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARGOAGVMGFPGPKGAAGEPGKAGERG
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 4.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM0038; COLFI; 1.
ROSITE; PS01208; VWFC_I; 1.
PROSITE; PS01208; VWFC_I; 1.
                                                                                                                                                                                                                               1445 AA; 137251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 -----GPTGLPGPPGERG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPGAKGL------
                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.6
Matches 516; Conservative
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728

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1089 GERGMKGHRĞFNGMQĞPPĞPPĞSĞEQĞAPĞPSĞPAĞPRĞPPĞSSĞSTĞKDĞVNĞLPĞPI 1148
GEPGAKGEPGPAGVQGPPGPSGEEGKRGSRGEPGPAGPPGPAGERGGPGSRGFPGSDGAS 488
                                                                                                                                                       GRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPP 357
                                                                                                                                                                                                                                                                                                        609 GPSGPSGERGEQGPAGSPGFQGLPGSPGPAGEAGKPGEQGAPGDAGGPGPSGPRGERGFP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GADGVAGPKGPAGERGSP-----GPACPKGSPGEAGRP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPAGPPGPSGEKGSPGSDGPAGAPGIPGPQGIAGQRGVVGLPGQRGEKGFSGLPGPAGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKQGPSGPNGERGPPGPPGPGLGGPPGEPGREGSPGSEGAPGRDGSPGPRGBNGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPKGAPGERGSVGPAGPKGSTGESGRPGEPGLPGAKGLTGSPGSPGPDGKTGPAGAAGQD
                                                                                                                                                                                        GHPGPPGPSGARGQSGVMGFPGPKGAAGEPGKSGERGVAGPPGATGAPGKDGEAGAQGPP
                                                                                                                                                                                                                                                                                                                                                                                                              669 GERGGOGPAGAOGPRGSPGSPGNDGAKGEAGAAGAPGGRGPPGLOGMPGERGSAGMPGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDRGDAGTKGADGAPGKDGARGLTGPIGPPGPSGAPGDKGEGGPSGPAGPTGARGSPGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849 GTRGAAGPPGATGFPGAAGRLGPPGPSGNAGPPGPPGPGGKEGAKGSRGETGPAGRSGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPAGPP---GEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVAGPKGPAGERGSPGPAGP-----GLT-KGSPGEAGRPGEAGLPGAK-----GLT
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                                                                                                                                                                                                                                                          GPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEAGLPGAKGLTGSPGS---PGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLP
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                                                    GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQD
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MEDLINE=22388257; PubMed=12477932;
Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Colla1-prov protein.
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                               ---PGERGGPGSRGFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1449 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPGEAGKPGEQGVPGDLGAPGPSGPAG
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NCBL TaxID=8355;
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GPAGPAGARGPSGPAGARGDKGEAGEQGERGMKGHRGFNDLPGPPGAPGHAGEQGPSGAS 1120
                                                                                                        GPAGPRGPPGSSGSPGKDGS---NGLPGPIGPPGPRGRTGDVGPAGPPGPAGPPGPP 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RC TISSUERNEE FROM N.A.

RC TISSUE-Regenerate forelimbs;

RX MEDINE-99407244; Pubmed=10474166;

RX MEDINE-999407244; Pubmed=10474166;

Asahina K., Obara M., Voshizato K.;

RXT mid development to fithe blastema of regenerating newt limb.";

DRV Dyn. 216:59-71(1999).

REMBL; AB015438; BAA36973.1; -.

RG; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0005701; F:phosphate transport; IEA.

InterPro; IPR00886; Fib_collagen_C.

R Ffam; PF01410; Collagen; 18.

PRODOM; PD00077; Clg_hellx; 4.

R ProDom; PD002078; Fib_collagen_C; 1.

R PRART; SM00218; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHRGFNGLDGAKGDNGPAGPKGEPGNPGENGAPGOAGPRGLPGERGRPGAPGPAGARGND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cynops pyrrhogaster (Japanese common newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1450 AA; 137563 MW; ABF8A74841B87B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                             olimarilass (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha I type I collagen.
Cynops pyrrhonnel
                                                         GPPGPAGPAGERGEOGPAGSPGFOGLPGPAGPPGEAGKPGE-
                                                                                                                                                                                                                                                                                                                                               PRT; 1450 AA
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PS50184; VWFC 2; 1.
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                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8330;
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PROSITE; PS50
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Matches
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390 641 447 701 501 757 558 587 875 645 702

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522 GAKGLTGSPGSPGSDGKTGPAGAPGQDGRAGPPGPPGARGQSGVMGFPGPKGAAGEPGKM
                                                                                                                                                                                                                                  GERGSPGPAGPKGSPGEAGRPGEAGLPGAK-----GLTGSPGSPGPDGKTGPPGPAGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 GAPGGOGPPGLOGMPGER---GSSGLPGAKGDRGDOGVKGSDGTPGKDGVRGLTGPIGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559 ------GPPGPAGPA-------GERGEQGPAGSPGFQGL----PGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 588 --AGPPGEAGKPGEQGVPGDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936 GPQGVAGSRGTVGLPGMRGERGFSGLPGPAGEPGKQGPSGPSGERGPPGPSGPPGLGGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GODGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996 GESGREGAPGSEGAPGRDGAVGPKGDRGEGGPAGPPGAPGAPGAPGPVGPAGKSGDRGET
                                               GAKGLIGSPGSPGPDGKTGPPGPAGQDGRPGPPGPPGARGQAGVMGFPGPKGAAGEPGKA
                                                                                                                                                                                  GERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEA
                                                                                                                                                                                                                                                                                                                         391 GKPGEQGVPGDLGAPGPSGPAGE---PGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPA
                                                                                                                                                                                                                                                                                                                                                                                           642 GKPGEQGVPGDVGPSGPAGARGERGFPGERGAQGPPGPQGARGSNGAPGNDGAKGEAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 GRPGPPGPPGARGQAGVMGFPGPKGAAGBPGKAGERGVPGPPGAVGPAGKDGEAGAQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 GDSGAKGDAGPPGPAGPTGAPGPAGALGSPGPKGARGAPGPPGATGFPGAAGRLGPPGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 GPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLPGAKGLTGSPGPGPDGKTGPP---GPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;
TISSUB-Mammary tumor. WAP-TGF alpha model. 7 months old;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuvik S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBL_TaxID=10090;
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27, Last sequence update)
27, Last annotation update)
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Q6PCL3;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
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Name=Collal;
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.J., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Grailska U., Samailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-EMDYON

Klein S., Strausberg R.;

BMBL; BC049829; AA449829.1; -.

BMBL; BC01000581; C:cotlagen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

GO; GO:0006517; P:phosphate transport; IEA.

InterPro; IPR008161; Cighelix.

InterPro; IPR008160; Collagen.

R InterPro; IPR001007; VWF—C.

Pfam; PF01410; COLFF; 1.

R Pfam; PF01410; Col.FF; 1.

R Pfam; PF010007; Cighelix; 4.

R Probom; PF000077; Cighelix; 4.

R Probom; PF000078; Fib collagen_C; 1.

R PRAMET; SM00289; COLFF; 1.

R SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 GPPGPAGPAGERGEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.
Richardson P.;
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54.6%; Pred. No. 6.7e-94;
ive 53; Mismatches 261; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01208; VWFC_1; UNKNOWN_1.
PROSITE; PS50184; VWFC_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dev. Dyn. 225:384-391(2002)
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nes 500; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Embryo;
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SEQUENCE
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630 GFQGLPGPPGBAGKPGBQGVPGDLGAPGPSGARGERGFPGBRGVQGPPGPAGPRGNN 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   870 GHRGFSGLQGPPGSPGEQGPSGASGPAGPRGPPGSAGSPGKDGLNGLPGPIGPPGPR 929
                                                     GFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAQGPPGPAGPAGERGEQGPAGSP
                                                                                                                                                                                                                                 690 GAPGNDGAKGDTGAPGAPGAPGELOGMPGERGAAGLPGPKGDAGDAGPKGADGSPGKD
                                                                                                                                                                                                                                                                                                                                              721 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGEAGAGGPPGPAGPAGERGE----
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                                                                                GFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGPAGE------PGP-----
                                                                                                                                                                                                    ------TGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPKGSPGE-
                                                                                                                                                                                                                                                                         669 -----AGRPGEAGLPGAKGLTGSPGSPGPDGKTGPPGPAGQDGRPGPPGARGQA
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AAHS9281;

02-MAR-2004 (TrEMBLrel. 27, Created)

02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

Collal protein.

Man musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=CSPBL/6J; TISSUE=Mammary tumor;
Strausbers R.;
Straitted (CCT-2003) to the EMBL/GenBank/DDBJ databases.
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id. Sci. U.S.A. 99:16899-16903(2002)
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 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 ---GFQGPPGEPGEPGGSGPWGPRGPPGKNGDDGEAGKPGRPGERGPPGPARGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GT---adargnogavgaagppgpr----gprgppgppgavgargaagpggar----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDLGAPGPSGPAGEPGPTGLPGPPGERGGPGSRGFPGADGVAGPKGPAGERGSPGPAGPK
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al Similarity 56.0%; Pred. No. 1.5e-92;
510; Conservative 29; Mismatches 227; Indels 144;
                                                                                                                                                                                                                                                                               A Strausberg R.;

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

R Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR008161; Fibrinogen.C.

R InterPro; IPR0008181; Fibrinogen.C.

R InterPro; IPR0008181; Fibrinogen.C.

R InterPro; IPR0008181; Fibrinogen.C.

R Pfam; PP01191; CoLF1; 1.

R Pfam; PP01391; CoLF1; 1.

R Pfam; PP01093; VWC; 1.

R Pfam; PP000093; VWC; 1.

R ProDom; PD000007; Clg helix; 2.

R ProDom; PD000007; Clg helix; 2.

R SMART; SM00031; VWC; 1.
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                             Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                 -TGPPGPAGQDGRPGPPGARGQA 108
                                                                                                                                                                                                                                          109 GVMGFPGPKGAAGEPGKAGERGVPGPPGAVGPAGKDGBAGAQGPP---GPAGPAGERGEQ 165
                                                                                                                                                                                                                                                                 189 ---GFQGPPGEPGEPGSGPMGPRGPPGPPGRNGDDGEAGKPGERGPPGPGGARGLP 245
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                                                                                                               12 PGPPGERGG-----PGSRGFPGADGVAGPKGPAGERGSPGPAGPKGSPGEAGRPGEAGLP
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                                                                                   Gaps
                                                                                   144;
                                              53.8%; Score 2494; DB 2; Length 1225; llarity 56.0%; Pred. No. 1.5e-92; Conservative 29; Mismatches 227; Indels 144
EMBL; BC059281; AAH59281.1; -. SEQUENCE 1225 AA; 117860 MW; B6B86CBB4457F4D9 CRC64;
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Matches 510; Conserv
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